

Jesse Lee Eickholt

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,275
citations

567281

15
h-index

677142

22
g-index

30
all docs

30
docs citations

30
times ranked

1578
citing authors

#	ARTICLE	IF	CITATIONS
1	A Deep Learning Network Approach to <i>ab initio</i> Protein Secondary Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 103-112.	3.0	254
2	Predicting protein residue-residue contacts using deep networks and boosting. <i>Bioinformatics</i> , 2012, 28, 3066-3072.	4.1	149
3	Improving Protein Fold Recognition by Deep Learning Networks. <i>Scientific Reports</i> , 2015, 5, 17573.	3.3	107
4	Machine Learning the Voltage of Electrode Materials in Metal-Ion Batteries. <i>ACS Applied Materials & Interfaces</i> , 2019, 11, 18494-18503.	8.0	104
5	PreDisorder: <i>ab initio</i> sequence-based prediction of protein disordered regions. <i>BMC Bioinformatics</i> , 2009, 10, 436.	2.6	92
6	A comprehensive overview of computational protein disorder prediction methods. <i>Molecular BioSystems</i> , 2012, 8, 114-121.	2.9	92
7	APOLLO: a quality assessment service for single and multiple protein models. <i>Bioinformatics</i> , 2011, 27, 1715-1716.	4.1	89
8	DNdisorder: predicting protein disorder using boosting and deep networks. <i>BMC Bioinformatics</i> , 2013, 14, 88.	2.6	74
9	DoBo: Protein domain boundary prediction by integrating evolutionary signals and machine learning. <i>BMC Bioinformatics</i> , 2011, 12, 43.	2.6	52
10	Machine Learning Screening of Metal-Ion Battery Electrode Materials. <i>ACS Applied Materials & Interfaces</i> , 2021, 13, 53355-53362.	8.0	42
11	Characterizing the Discussion of Antibiotics in the Twittersphere: What is the Bigger Picture?. <i>Journal of Medical Internet Research</i> , 2015, 17, e154.	4.3	34
12	The MULTICOM toolbox for protein structure prediction. <i>BMC Bioinformatics</i> , 2012, 13, 65.	2.6	30
13	Designing and benchmarking the MULTICOM protein structure prediction system. <i>BMC Structural Biology</i> , 2013, 13, 2.	2.3	25
14	Benchmarking Deep Networks for Predicting Residue-Specific Quality of Individual Protein Models in CASP11. <i>Scientific Reports</i> , 2016, 6, 19301.	3.3	22
15	Applications of deep convolutional neural networks to predict length, circumference, and weight from mostly dewatered images of fish. <i>Ecology and Evolution</i> , 2020, 10, 9313-9325.	1.9	20
16	A conformation ensemble approach to protein residue-residue contact. <i>BMC Structural Biology</i> , 2011, 11, 38.	2.3	15
17	An Overview of Practical Applications of Protein Disorder Prediction and Drive for Faster, More Accurate Predictions. <i>International Journal of Molecular Sciences</i> , 2015, 16, 15384-15404.	4.1	15
18	Practical Active Learning Stations to Transform Existing Learning Environments Into Flexible, Active Learning Classrooms. <i>IEEE Transactions on Education</i> , 2021, 64, 95-102.	2.4	15

#	ARTICLE	IF	CITATIONS
19	Advancements towards selective barrier passage by automatic species identification: applications of deep convolutional neural networks on images of dewatered fish. ICES Journal of Marine Science, 2020, 77, 2804-2813.	2.5	12
20	Levels of active learning in programming skill acquisition: From lecture to active learning rooms. , 2017, , .		7
21	A distributed pipeline for DIDSON data processing. , 2017, , .		5
22	Recursive protein modeling: A divide and conquer strategy for protein structure prediction and its case study in CASP9. , 2011, , .		4
23	TopQA: a topological representation for single-model protein quality assessment with machine learning. International Journal of Computational Biology and Drug Design, 2020, 13, 144.	0.3	4
24	Creating Economy Active Learning Classrooms for IT Students. , 2017, , .		3
25	Supporting Project-Based Learning through Economical and Flexible Learning Spaces. Education Sciences, 2019, 9, 212.	2.6	3
26	Supporting active learning through commodity and open source solutions. , 2017, , .		2
27	Low-Cost Active Learning Benefits for Introductory Computer Science Courses. , 2019, , .		2
28	PCP-ML: Protein characterization package for machine learning. BMC Research Notes, 2014, 7, 810.	1.4	1
29	Advancing Adoption of Active Learning Pedagogy via New Avenues of Research and Training. , 2019, , .		1
30	Adopting the MapReduce framework to pre-train 1-D and 2-D protein structure predictors with large protein datasets. , 2014, , .		0