

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	Practical Active Learning Stations to Transform Existing Learning Environments Into Flexible, Active Learning Classrooms. IEEE Transactions on Education, 2021, 64, 95-102.	2.4	15
2	Machine Learning Screening of Metal-Ion Battery Electrode Materials. ACS Applied Materials & Interfaces, 2021, 13, 53355-53362.	8.0	42
3	Applications of deep convolutional neural networks to predict length, circumference, and weight from mostly dewatered images of fish. Ecology and Evolution, 2020, 10, 9313-9325.	1.9	20
4	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
5	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
6	Supporting Project-Based Learning through Economical and Flexible Learning Spaces. Education Sciences, 2019, 9, 212.	2.6	3
7	Machine Learning the Voltage of Electrode Materials in Metal-Ion Batteries. ACS Applied Materials & Interfaces, 2019, 11, 18494-18503.	8.0	104
8	Advancing Adoption of Active Learning Pedagogy via New Avenues of Research and Training. , 2019, , .		1
9	Low-Cost Active Learning Benefits for Introductory Computer Science Courses. , 2019, , .		2
10	A distributed pipeline for DIDSON data processing. , 2017, , .		5
11	Levels of active learning in programming skill acquisition: From lecture to active learning rooms. , 2017, , .		7
12	Supporting active learning through commodity and open source solutions. , 2017, , .		2
13	Creating Economy Active Learning Classrooms for IT Students. , 2017, , .		3
14	Benchmarking Deep Networks for Predicting Residue-Specific Quality of Individual Protein Models in CASP11. Scientific Reports, 2016, 6, 19301.	3.3	22
15	Improving Protein Fold Recognition by Deep Learning Networks. Scientific Reports, 2015, 5, 17573.	3.3	107
16	An Overview of Practical Applications of Protein Disorder Prediction and Drive for Faster, More Accurate Predictions. International Journal of Molecular Sciences, 2015, 16, 15384-15404.	4.1	15
17	A Deep Learning Network Approach to <i>ab initio</i> Protein Secondary Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 103-112.	3.0	254
18	Characterizing the Discussion of Antibiotics in the Twittersphere: What is the Bigger Picture?. Journal of Medical Internet Research, 2015, 17, e154.	4.3	34

#	ARTICLE	IF	CITATIONS
19	PCP-ML: Protein characterization package for machine learning. BMC Research Notes, 2014, 7, 810.	1.4	1
20	Adopting the MapReduce framework to pre-train 1-D and 2-D protein structure predictors with large protein datasets. , 2014, , .		0
21	DNdisorder: predicting protein disorder using boosting and deep networks. BMC Bioinformatics, 2013, 14, 88.	2.6	74
22	Designing and benchmarking the MULTICOM protein structure prediction system. BMC Structural Biology, 2013, 13, 2.	2.3	25
23	Predicting protein residue-residue contacts using deep networks and boosting. Bioinformatics, 2012, 28, 3066-3072.	4.1	149
24	A comprehensive overview of computational protein disorder prediction methods. Molecular BioSystems, 2012, 8, 114-121.	2.9	92
25	The MULTICOM toolbox for protein structure prediction. BMC Bioinformatics, 2012, 13, 65.	2.6	30
26	Recursive protein modeling: A divide and conquer strategy for protein structure prediction and its case study in CASP9. , 2011, , .		4
27	A conformation ensemble approach to protein residue-residue contact. BMC Structural Biology, 2011, 11, 38.	2.3	15
28	DoBo: Protein domain boundary prediction by integrating evolutionary signals and machine learning. BMC Bioinformatics, 2011, 12, 43.	2.6	52
29	APOLLO: a quality assessment service for single and multiple protein models. Bioinformatics, 2011, 27, 1715-1716.	4.1	89
30	PreDisorder: ab initio sequence-based prediction of protein disordered regions. BMC Bioinformatics, 2009, 10, 436.	2.6	92