Rhys Heffernan

List of Publications by Year
in descending order

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12 papers	1,565 citations	759055 12 h-index	1199470 12 g-index
12 all docs	12 docs citations	12 times ranked	1628 citing authors

#	Article	IF	Citations
1	Capturing non-local interactions by long short-term memory bidirectional recurrent neural networks for improving prediction of protein secondary structure, backbone angles, contact numbers and solvent accessibility. Bioinformatics, 2017, 33, 2842-2849.	1.8	300
2	Improving prediction of secondary structure, local backbone angles and solvent accessible surface area of proteins by iterative deep learning. Scientific Reports, 2015, 5, 11476.	1.6	290
3	Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Choux×³s general PseAAC. Journal of Theoretical Biology, 2015, 364, 284-294.	0.8	232
4	Sixty-five years of the long march in protein secondary structure prediction: the final stretch?. Briefings in Bioinformatics, 2018, 19, bbw129.	3.2	168
5	SPIDER2: A Package to Predict Secondary Structure, Accessible Surface Area, and Main-Chain Torsional Angles by Deep Neural Networks. Methods in Molecular Biology, 2017, 1484, 55-63.	0.4	137
6	Predicting backbone CÎ± angles and dihedrals from protein sequences by stacked sparse autoâ€encoder deep neural network. Journal of Computational Chemistry, 2014, 35, 2040-2046.	1.5	133
7	Singleâ€sequenceâ€based prediction of protein secondary structures and solvent accessibility by deep wholeâ€sequence learning. Journal of Computational Chemistry, 2018, 39, 2210-2216.	1.5	84
8	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. Bioinformatics, 2016, 32, 843-849.	1.8	79
9	SPIN2: Predicting sequence profiles from protein structures using deep neural networks. Proteins: Structure, Function and Bioinformatics, 2018, 86, 629-633.	1.5	62
10	Advancing the Accuracy of Protein Fold Recognition by Utilizing Profiles From Hidden Markov Models. IEEE Transactions on Nanobioscience, 2015, 14, 761-772.	2.2	34
11	Protein fold recognition using HMMâ€“HMM alignment and dynamic programming. Journal of Theoretical Biology, 2016, 393, 67-74.	0.8	33
12	Detecting Proline and Non-Proline Cis Isomers in Protein Structures from Sequences Using Deep Residual Ensemble Learning. Journal of Chemical Information and Modeling, 2018, 58, 2033-2042.	2.5	13