

Ghazaleh Taherzadeh

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

540
citations

840776

11
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996975

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all docs

15
docs citations

15
times ranked

483
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence-based prediction of protein-peptide binding sites using support vector machine. <i>Journal of Computational Chemistry</i> , 2016, 37, 1223-1229.	3.3	81
2	PSSM-Suc: Accurately predicting succinylation using position specific scoring matrix into bigram for feature extraction. <i>Journal of Theoretical Biology</i> , 2017, 425, 97-102.	1.7	65
3	Structure-based prediction of protein-peptide binding regions using Random Forest. <i>Bioinformatics</i> , 2018, 34, 477-484.	4.1	62
4	Sequence-Based Prediction of Protein-Carbohydrate Binding Sites Using Support Vector Machines. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 2115-2122.	5.4	59
5	SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. <i>Analytical Biochemistry</i> , 2017, 527, 24-32.	2.4	55
6	Improving succinylation prediction accuracy by incorporating the secondary structure via helix, strand and coil, and evolutionary information from profile bigrams. <i>PLoS ONE</i> , 2018, 13, e0191900.	2.5	51
7	SPRINT-Gly: predicting N- and O-linked glycosylation sites of human and mouse proteins by using sequence and predicted structural properties. <i>Bioinformatics</i> , 2019, 35, 4140-4146.	4.1	48
8	Predicting lysine malonylation sites of proteins using sequence and predicted structural features. <i>Journal of Computational Chemistry</i> , 2018, 39, 1757-1763.	3.3	30
9	Predicting protein-peptide binding sites with a deep convolutional neural network. <i>Journal of Theoretical Biology</i> , 2020, 496, 110278.	1.7	25
10	Accurately Predicting Glutarylation Sites Using Sequential Bi-Peptide-Based Evolutionary Features. <i>Genes</i> , 2020, 11, 1023.	2.4	17
11	SumSec: Accurate Prediction of Sumoylation Sites Using Predicted Secondary Structure. <i>Molecules</i> , 2018, 23, 3260.	3.8	13
12	Mal-Light: Enhancing Lysine Malonylation Sites Prediction Problem Using Evolutionary-based Features. <i>IEEE Access</i> , 2020, 8, 77888-77902.	4.2	12
13	Accurate prediction of RNA 5-hydroxymethylcytosine modification by utilizing novel position-specific gapped k-mer descriptors. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3528-3538.	4.1	11
14	SEMal: Accurate protein malonylation site predictor using structural and evolutionary information. <i>Computers in Biology and Medicine</i> , 2020, 125, 104022.	7.0	10
15	Computational Prediction of N- and O-Linked Glycosylation Sites for Human and Mouse Proteins. <i>Methods in Molecular Biology</i> , 2022, , 177-186.	0.9	1