Md Mehedi Hasan

List of Publications by Year
in descending order

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33	1,178	304368	433756
papers	citations	22 h-index	31 g-index

34	34	34	536
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	BERT6mA: prediction of DNA N6-methyladenine site using deep learning-based approaches. Briefings in Bioinformatics, 2022, 23, .	3.2	23
2	DeepDNAbP: A deep learning-based hybrid approach to improve the identification of deoxyribonucleic acid-binding proteins. Computers in Biology and Medicine, 2022, 145, 105433.	3.9	5
3	Deepm5C: A deep-learning-based hybrid framework for identifying human RNA N5-methylcytosine sites using a stacking strategy. Molecular Therapy, 2022, 30, 2856-2867.	3.7	40
4	TACOS: a novel approach for accurate prediction of cell-specific long noncoding RNAs subcellular localization. Briefings in Bioinformatics, 2022, 23, .	3.2	21
5	iAMY-SCM: Improved prediction and analysis of amyloid proteins using a scoring card method with propensity scores of dipeptides. Genomics, 2021, 113, 689-698.	1.3	31
6	Critical evaluation of web-based DNA N6-methyladenine site prediction tools. Briefings in Functional Genomics, 2021, 20, 258-272.	1.3	29
7	Improved Prediction of Protein-Protein Interaction Mapping on Homo Sapiens by Using Amino Acid Sequence Features in a Supervised Learning Framework. Protein and Peptide Letters, 2021, 28, 74-83.	0.4	4
8	IRC-Fuse: improved and robust prediction of redox-sensitive cysteine by fusing of multiple feature representations. Journal of Computer-Aided Molecular Design, 2021, 35, 315-323.	1.3	5
9	In Silico Approaches for the Prediction and Analysis of Antiviral Peptides: A Review. Current Pharmaceutical Design, 2021, 27, 2180-2188.	0.9	18
10	Integrative machine learning framework for the identification of cell-specific enhancers from the human genome. Briefings in Bioinformatics, 2021, 22, .	3.2	38
11	iBitter-Fuse: A Novel Sequence-Based Bitter Peptide Predictor by Fusing Multi-View Features. International Journal of Molecular Sciences, 2021, 22, 8958.	1.8	27
12	UMPred-FRL: A New Approach for Accurate Prediction of Umami Peptides Using Feature Representation Learning. International Journal of Molecular Sciences, 2021, 22, 13124.	1.8	35
13	i4mC-ROSE, a bioinformatics tool for the identification of DNA N4-methylcytosine sites in the Rosaceae genome. International Journal of Biological Macromolecules, 2020, 157, 752-758.	3.6	74
14	Empirical Comparison and Analysis of Web-Based DNA N4-Methylcytosine Site Prediction Tools. Molecular Therapy - Nucleic Acids, 2020, 22, 406-420.	2.3	38
15	iUmami-SCM: A Novel Sequence-Based Predictor for Prediction and Analysis of Umami Peptides Using a Scoring Card Method with Propensity Scores of Dipeptides. Journal of Chemical Information and Modeling, 2020, 60, 6666-6678.	2.5	76
16	iLBE for Computational Identification of Linear B-cell Epitopes by Integrating Sequence and Evolutionary Features. Genomics, Proteomics and Bioinformatics, 2020, 18, 593-600.	3.0	30
17	ProIn-Fuse: improved and robust prediction of proinflammatory peptides by fusing of multiple feature representations. Journal of Computer-Aided Molecular Design, 2020, 34, 1229-1236.	1.3	33
18	iDPPIV-SCM: A Sequence-Based Predictor for Identifying and Analyzing Dipeptidyl Peptidase IV (DPP-IV) Inhibitory Peptides Using a Scoring Card Method. Journal of Proteome Research, 2020, 19, 4125-4136.	1.8	66

#	Article	IF	Citations
19	iTTCA-Hybrid: Improved and robust identification of tumor T cell antigens by utilizing hybrid feature representation. Analytical Biochemistry, 2020, 599, 113747.	1.1	40
20	Meta-iPVP: a sequence-based meta-predictor for improving the prediction of phage virion proteins using effective feature representation. Journal of Computer-Aided Molecular Design, 2020, 34, 1105-1116.	1.3	51
21	i4mC-Mouse: Improved identification of DNA N4-methylcytosine sites in the mouse genome using multiple encoding schemes. Computational and Structural Biotechnology Journal, 2020, 18, 906-912.	1.9	57
22	iBitter-SCM: Identification and characterization of bitter peptides using a scoring card method with propensity scores of dipeptides. Genomics, 2020, 112, 2813-2822.	1.3	77
23	Recent Development of Machine Learning Methods in Microbial Phosphorylation Sites. Current Genomics, 2020, 21, 194-203.	0.7	8
24	Evolution of Sequence-based Bioinformatics Tools for Protein-protein Interaction Prediction. Current Genomics, 2020, 21, 454-463.	0.7	25
25	Computational identification of microbial phosphorylation sites by the enhanced characteristics of sequence information. Scientific Reports, 2019, 9, 8258.	1.6	32
26	Large-Scale Assessment of Bioinformatics Tools for Lysine Succinylation Sites. Cells, 2019, 8, 95.	1.8	42
27	Prediction of S-nitrosylation sites by integrating support vector machines and random forest. Molecular Omics, 2019, 15, 451-458.	1.4	48
28	SIPMA: A Systematic Identification of Protein-Protein Interactions in Zea mays Using Autocorrelation Features in a Machine-Learning Framework. , 2018, , .		6
29	iLMS, Computational Identification of Lysine-Malonylation Sites by Combining Multiple Sequence Features. , 2018, , .		5
30	NTyroSite: Computational Identification of Protein Nitrotyrosine Sites Using Sequence Evolutionary Features. Molecules, 2018, 23, 1667.	1.7	35
31	Computational Modeling of Lysine Post-Translational Modification: An Overview. Current Synthetic and Systems Biology, 2018, 06, .	0.3	7
32	Computational identification of protein S-sulfenylation sites by incorporating the multiple sequence features information. Molecular BioSystems, 2017, 13, 2545-2550.	2.9	56
33	SuccinSite: a computational tool for the prediction of protein succinylation sites by exploiting the amino acid patterns and properties. Molecular BioSystems, 2016, 12, 786-795.	2.9	93