

Md Mehedi Hasan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9551946/publications.pdf>

Version: 2024-02-01

33
papers

1,178
citations

304368

22
h-index

433756

31
g-index

34
all docs

34
docs citations

34
times ranked

536
citing authors

#	ARTICLE	IF	CITATIONS
1	SuccinSite: a computational tool for the prediction of protein succinylation sites by exploiting the amino acid patterns and properties. <i>Molecular BioSystems</i> , 2016, 12, 786-795.	2.9	93
2	iBitter-SCM: Identification and characterization of bitter peptides using a scoring card method with propensity scores of dipeptides. <i>Genomics</i> , 2020, 112, 2813-2822.	1.3	77
3	iUmami-SCM: A Novel Sequence-Based Predictor for Prediction and Analysis of Umami Peptides Using a Scoring Card Method with Propensity Scores of Dipeptides. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 6666-6678.	2.5	76
4	i4mC-ROSE, a bioinformatics tool for the identification of DNA N4-methylcytosine sites in the Rosaceae genome. <i>International Journal of Biological Macromolecules</i> , 2020, 157, 752-758.	3.6	74
5	iDPPIV-SCM: A Sequence-Based Predictor for Identifying and Analyzing Dipeptidyl Peptidase IV (DPP-IV) Inhibitory Peptides Using a Scoring Card Method. <i>Journal of Proteome Research</i> , 2020, 19, 4125-4136.	1.8	66
6	i4mC-Mouse: Improved identification of DNA N4-methylcytosine sites in the mouse genome using multiple encoding schemes. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 906-912.	1.9	57
7	Computational identification of protein S-sulfenylation sites by incorporating the multiple sequence features information. <i>Molecular BioSystems</i> , 2017, 13, 2545-2550.	2.9	56
8	Meta-iPVP: a sequence-based meta-predictor for improving the prediction of phage virion proteins using effective feature representation. <i>Journal of Computer-Aided Molecular Design</i> , 2020, 34, 1105-1116.	1.3	51
9	Prediction of <i>S</i>-nitrosylation sites by integrating support vector machines and random forest. <i>Molecular Omics</i> , 2019, 15, 451-458.	1.4	48
10	Large-Scale Assessment of Bioinformatics Tools for Lysine Succinylation Sites. <i>Cells</i> , 2019, 8, 95.	1.8	42
11	iTTCA-Hybrid: Improved and robust identification of tumor T cell antigens by utilizing hybrid feature representation. <i>Analytical Biochemistry</i> , 2020, 599, 113747.	1.1	40
12	Deepm5C: A deep-learning-based hybrid framework for identifying human RNA N5-methylcytosine sites using a stacking strategy. <i>Molecular Therapy</i> , 2022, 30, 2856-2867.	3.7	40
13	Empirical Comparison and Analysis of Web-Based DNA N4-Methylcytosine Site Prediction Tools. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 22, 406-420.	2.3	38
14	Integrative machine learning framework for the identification of cell-specific enhancers from the human genome. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	38
15	NTyroSite: Computational Identification of Protein Nitrotyrosine Sites Using Sequence Evolutionary Features. <i>Molecules</i> , 2018, 23, 1667.	1.7	35
16	UMPred-FRL: A New Approach for Accurate Prediction of Umami Peptides Using Feature Representation Learning. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13124.	1.8	35
17	ProIn-Fuse: improved and robust prediction of proinflammatory peptides by fusing of multiple feature representations. <i>Journal of Computer-Aided Molecular Design</i> , 2020, 34, 1229-1236.	1.3	33
18	Computational identification of microbial phosphorylation sites by the enhanced characteristics of sequence information. <i>Scientific Reports</i> , 2019, 9, 8258.	1.6	32

#	ARTICLE	IF	CITATIONS
19	iAMY-SCM: Improved prediction and analysis of amyloid proteins using a scoring card method with propensity scores of dipeptides. <i>Genomics</i> , 2021, 113, 689-698.	1.3	31
20	iLBE for Computational Identification of Linear B-cell Epitopes by Integrating Sequence and Evolutionary Features. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 593-600.	3.0	30
21	Critical evaluation of web-based DNA N6-methyladenine site prediction tools. <i>Briefings in Functional Genomics</i> , 2021, 20, 258-272.	1.3	29
22	iBitter-Fuse: A Novel Sequence-Based Bitter Peptide Predictor by Fusing Multi-View Features. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8958.	1.8	27
23	Evolution of Sequence-based Bioinformatics Tools for Protein-protein Interaction Prediction. <i>Current Genomics</i> , 2020, 21, 454-463.	0.7	25
24	BERT6mA: prediction of DNA N6-methyladenine site using deep learning-based approaches. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	23
25	TACOS: a novel approach for accurate prediction of cell-specific long noncoding RNAs subcellular localization. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	21
26	In Silico Approaches for the Prediction and Analysis of Antiviral Peptides: A Review. <i>Current Pharmaceutical Design</i> , 2021, 27, 2180-2188.	0.9	18
27	Recent Development of Machine Learning Methods in Microbial Phosphorylation Sites. <i>Current Genomics</i> , 2020, 21, 194-203.	0.7	8
28	Computational Modeling of Lysine Post-Translational Modification: An Overview. <i>Current Synthetic and Systems Biology</i> , 2018, 06, .	0.3	7
29	SIPMA: A Systematic Identification of Protein-Protein Interactions in <i>Zea mays</i> Using Autocorrelation Features in a Machine-Learning Framework. , 2018, , .		6
30	iLMS, Computational Identification of Lysine-Malonylation Sites by Combining Multiple Sequence Features. , 2018, , .		5
31	IRC-Fuse: improved and robust prediction of redox-sensitive cysteine by fusing of multiple feature representations. <i>Journal of Computer-Aided Molecular Design</i> , 2021, 35, 315-323.	1.3	5
32	DeepDNAbP: A deep learning-based hybrid approach to improve the identification of deoxyribonucleic acid-binding proteins. <i>Computers in Biology and Medicine</i> , 2022, 145, 105433.	3.9	5
33	Improved Prediction of Protein-Protein Interaction Mapping on <i>Homo Sapiens</i> by Using Amino Acid Sequence Features in a Supervised Learning Framework. <i>Protein and Peptide Letters</i> , 2021, 28, 74-83.	0.4	4