Robert H Newman

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4246336/publications.pdf

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840776 888059 23 322 11 citations h-index g-index papers

25 25 25 359 docs citations times ranked citing authors all docs

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#	Article	IF	CITATIONS
1	DeepSuccinylSite: a deep learning based approach for protein succinylation site prediction. BMC Bioinformatics, 2020, 21, 63.	2.6	45
2	Toward a systems-level view of dynamic phosphorylation networks. Frontiers in Genetics, 2014, 5, 263.	2.3	36
3	RF-Phos: A Novel General Phosphorylation Site Prediction Tool Based on Random Forest. BioMed Research International, 2016, 2016, 1-12.	1.9	34
4	RF-GlutarySite: a random forest based predictor for glutarylation sites. Molecular Omics, 2019, 15, 189-204.	2.8	30
5	RF-Hydroxysite: a random forest based predictor for hydroxylation sites. Molecular BioSystems, 2016, 12, 2427-2435.	2.9	24
6	SARS-COV-2, infection, transmission, transcription, translation, proteins, and treatment: A review. International Journal of Biological Macromolecules, 2021, 193, 1249-1273.	7.5	19
7	DeepRMethylSite: a deep learning based approach for prediction of arginine methylation sites in proteins. Molecular Omics, 2020, 16, 448-454.	2.8	18
8	Isoform-specific interactions between meprin metalloproteases and the catalytic subunit of protein kinase A: significance in acute and chronic kidney injury. American Journal of Physiology - Renal Physiology, 2015, 308, F56-F68.	2.7	15
9	SVM-SulfoSite: A support vector machine based predictor for sulfenylation sites. Scientific Reports, 2018, 8, 11288.	3.3	14
10	RF-MaloSite and DL-Malosite: Methods based on random forest and deep learning to identify malonylation sites. Computational and Structural Biotechnology Journal, 2020, 18, 852-860.	4.1	14
11	Computational Analysis of the Binding Mechanism of GenX and HSA. ACS Omega, 2021, 6, 29166-29170.	3.5	14
12	DTL-DephosSite: Deep Transfer Learning Based Approach to Predict Dephosphorylation Sites. Frontiers in Cell and Developmental Biology, 2021, 9, 662983.	3.7	12
13	Inflammation and Kidney Injury in Diabetic African American Men. Journal of Diabetes Research, 2019, 2019, 1-12.	2.3	11
14	A deep learning based approach for prediction of Chlamydomonas reinhardtii phosphorylation sites. Scientific Reports, 2021, 11, 12550.	3.3	10
15	BCATc modulates crosstalk between the PI3K/Akt and the Ras/ERK pathway regulating proliferation in triple negative breast cancer. Oncotarget, 2020, 11, 1971-1987.	1.8	10
16	Introducing Chemistry Students to Emerging Technologies in Gene Editing, Their Applications, and Ethical Considerations. Journal of Chemical Education, 2020, 97, 1931-1943.	2.3	5
17	Undiagnosed Kidney Injury in Uninsured and Underinsured Diabetic African American Men and Putative Role of Meprin Metalloproteases in Diabetic Nephropathy. International Journal of Nephrology, 2018, 2018, 1-16.	1.3	4
18	Natural and synthetic pathogen associated molecular patterns modulate galectin expression in cow blood. Journal of Animal Science and Technology, 2019, 61, 245-253.	2.5	4

#	Article	IF	CITATIONS
19	FEPS: A Tool for Feature Extraction from Protein Sequence. Methods in Molecular Biology, 2022, , 65-104.	0.9	3
20	Performance of Canonical Correlation Forest in Phosphorylation Site Predictions., 2018,,.		0
21	Impact of Redox Modification on Protein Kinase A (PKA) and Mitogen Activated Protein Kinase 1 (MAPK1) Substrate Selection. FASEB Journal, 2021, 35, .	0.5	O
22	Impact of Redox Modification on MAPK Global Substrate Selection. FASEB Journal, 2022, 36, .	0.5	0
23	Impact of Redox Modification on PKA Substrate Selection. FASEB Journal, 2022, 36, .	0.5	0