

Robert H Newman

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

322
citations

840776

11
h-index

888059

17
g-index

25
all docs

25
docs citations

25
times ranked

359
citing authors

#	ARTICLE	IF	CITATIONS
1	Impact of Redox Modification on MAPK Global Substrate Selection. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
2	Impact of Redox Modification on PKA Substrate Selection. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
3	FEPS: A Tool for Feature Extraction from Protein Sequence. <i>Methods in Molecular Biology</i> , 2022, , 65-104.	0.9	3
4	Impact of Redox Modification on Protein Kinase A (PKA) and Mitogen Activated Protein Kinase 1 (MAPK1) Substrate Selection. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
5	DTL-DephosSite: Deep Transfer Learning Based Approach to Predict Dephosphorylation Sites. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 662983.	3.7	12
6	A deep learning based approach for prediction of <i>Chlamydomonas reinhardtii</i> phosphorylation sites. <i>Scientific Reports</i> , 2021, 11, 12550.	3.3	10
7	SARS-COV-2, infection, transmission, transcription, translation, proteins, and treatment: A review. <i>International Journal of Biological Macromolecules</i> , 2021, 193, 1249-1273.	7.5	19
8	Computational Analysis of the Binding Mechanism of GenX and HSA. <i>ACS Omega</i> , 2021, 6, 29166-29170.	3.5	14
9	Introducing Chemistry Students to Emerging Technologies in Gene Editing, Their Applications, and Ethical Considerations. <i>Journal of Chemical Education</i> , 2020, 97, 1931-1943.	2.3	5
10	DeepRMethylSite: a deep learning based approach for prediction of arginine methylation sites in proteins. <i>Molecular Omics</i> , 2020, 16, 448-454.	2.8	18
11	RF-MaloSite and DL-Malosite: Methods based on random forest and deep learning to identify malonylation sites. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 852-860.	4.1	14
12	DeepSuccinylSite: a deep learning based approach for protein succinylation site prediction. <i>BMC Bioinformatics</i> , 2020, 21, 63.	2.6	45
13	BCATc modulates crosstalk between the PI3K/Akt and the Ras/ERK pathway regulating proliferation in triple negative breast cancer. <i>Oncotarget</i> , 2020, 11, 1971-1987.	1.8	10
14	RF-GlutarySite: a random forest based predictor for glutarylation sites. <i>Molecular Omics</i> , 2019, 15, 189-204.	2.8	30
15	Inflammation and Kidney Injury in Diabetic African American Men. <i>Journal of Diabetes Research</i> , 2019, 2019, 1-12.	2.3	11
16	Natural and synthetic pathogen associated molecular patterns modulate galectin expression in cow blood. <i>Journal of Animal Science and Technology</i> , 2019, 61, 245-253.	2.5	4
17	Performance of Canonical Correlation Forest in Phosphorylation Site Predictions. , 2018, , .		0
18	Undiagnosed Kidney Injury in Uninsured and Underinsured Diabetic African American Men and Putative Role of Meprin Metalloproteases in Diabetic Nephropathy. <i>International Journal of Nephrology</i> , 2018, 2018, 1-16.	1.3	4

#	ARTICLE	IF	CITATIONS
19	SVM-SulfoSite: A support vector machine based predictor for sulfenylation sites. Scientific Reports, 2018, 8, 11288.	3.3	14
20	RF-Phos: A Novel General Phosphorylation Site Prediction Tool Based on Random Forest. BioMed Research International, 2016, 2016, 1-12.	1.9	34
21	RF-Hydroxysite: a random forest based predictor for hydroxylation sites. Molecular BioSystems, 2016, 12, 2427-2435.	2.9	24
22	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
23	Toward a systems-level view of dynamic phosphorylation networks. Frontiers in Genetics, 2014, 5, 263.	2.3	36