

# Hafeez Ur Rehman

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3059195/publications.pdf>

Version: 2024-02-01

17  
papers

712  
citations

1478505

6  
h-index

1281871

11  
g-index

18  
all docs

18  
docs citations

18  
times ranked

875  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Ontology GAN (GOGAN): a novel architecture for protein function prediction. <i>Soft Computing</i> , 2022, 26, 7653-7667.	3.6	7
2	m6A-Finder: Detecting m6A methylation sites from RNA transcriptomes using physical and statistical properties based features. <i>Computational Biology and Chemistry</i> , 2022, 97, 107640.	2.3	5
3	Gradient Compass-Based Adaptive Multimodal Medical Image Fusion. <i>IEEE Access</i> , 2021, 9, 22662-22670.	4.2	6
4	Detecting N6-methyladenosine sites from RNA transcriptomes using random forest. <i>Journal of Computational Science</i> , 2020, 47, 101238.	2.9	6
5	Beyond Homology Transfer: Deep Learning for Automated Annotation of Proteins. <i>Journal of Grid Computing</i> , 2019, 17, 225-237.	3.9	29
6	A Deep Learning based Approach for Precise Video Tagging. , 2019, , .		8
7	Evaluation of Multi-Modal MRI Images for Brain Tumor Segmentation. , 2019, , .		3
8	BSite-pro: A Novel Approach for Binding Site Prediction in Protein Sequences. , 2019, , .		0
9	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
10	A Bayesian approach for estimating protein-protein interactions by integrating structural and non-structural biological data. <i>Molecular BioSystems</i> , 2017, 13, 2592-2602.	2.9	1
11	A three-way approach for protein function classification. <i>PLoS ONE</i> , 2017, 12, e0171702.	2.5	11
12	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
13	A Three-Way Decision Making Approach to Protein Functions Classification. , 2016, , .		0
14	A Structure based Approach for Accurate Prediction of Protein Interactions Networks. , 2016, , .		7
15	Using Boolean networks to model post-transcriptional regulation in gene regulatory networks. <i>Journal of Computational Science</i> , 2014, 5, 332-344.	2.9	22
16	A combined approach for genome wide protein function annotation/prediction. <i>Proteome Science</i> , 2013, 11, S1.	1.7	22
17	Combining homolog and motif similarity data with Gene Ontology relationships for protein function prediction. , 2012, , .		9