

# Fahad Saeed

## List of Publications by Year in descending order

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Version: 2024-02-01

67  
papers

1,415  
citations

567281

15  
h-index

377865

34  
g-index

71  
all docs

71  
docs citations

71  
times ranked

1326  
citing authors

#	ARTICLE	IF	CITATIONS
1	Communication lower-bounds for distributed-memory computations for mass spectrometry based omics data. <i>Journal of Parallel and Distributed Computing</i> , 2022, 161, 37-47.	4.1	2
2	Unsupervised Structural Classification of Dissolved Organic Matter Based on Fragmentation Pathways. <i>Environmental Science &amp; Technology</i> , 2022, 56, 1458-1468.	10.0	12
3	Biomedical IoT: Enabling Technologies, Architectural Elements, Challenges, and Future Directions. <i>IEEE Access</i> , 2022, 10, 31306-31339.	4.2	21
4	A Deep Learning-Based Data Minimization Algorithm for Fast and Secure Transfer of Big Genomic Datasets. <i>IEEE Transactions on Big Data</i> , 2021, 7, 271-284.	6.1	9
5	Methods for Proteogenomics Data Analysis, Challenges, and Scalability Bottlenecks: A Survey. <i>IEEE Access</i> , 2021, 9, 5497-5516.	4.2	14
6	Explainable and scalable machine learning algorithms for detection of autism spectrum disorder using fMRI data. , 2021, , 39-54.		7
7	Benchmarking mass spectrometry based proteomics algorithms using a simulated database. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2021, 10, 1.	2.1	0
8	ASD-SAENet: A Sparse Autoencoder, and Deep-Neural Network Model for Detecting Autism Spectrum Disorder (ASD) Using fMRI Data. <i>Frontiers in Computational Neuroscience</i> , 2021, 15, 654315.	2.1	49
9	High performance computing framework for tera-scale database search of mass spectrometry data. <i>Nature Computational Science</i> , 2021, 1, 550-561.	8.0	7
10	Communication-avoiding micro-architecture to compute Xcorr scores for peptide identification. , 2021, 2021, 99-103.		1
11	SpeCollate: Deep cross-modal similarity network for mass spectrometry data based peptide deductions. <i>PLoS ONE</i> , 2021, 16, e0259349.	2.5	6
12	DeepCOVIDNet: Deep Convolutional Neural Network for COVID-19 Detection from Chest Radiographic Images. , 2021, 2021, 1703-1710.		1
13	NGS-Integrator: An efficient tool for combining multiple NGS data tracks using minimum Bayesâ€™ factors. <i>BMC Genomics</i> , 2020, 21, 806.	2.8	3
14	Federated Learning: A Survey on Enabling Technologies, Protocols, and Applications. <i>IEEE Access</i> , 2020, 8, 140699-140725.	4.2	313
15	Machine Learning Methods for Diagnosing Autism Spectrum Disorder and Attention-Deficit/Hyperactivity Disorder Using Functional and Structural MRI: A Survey. <i>Frontiers in Neuroinformatics</i> , 2020, 14, 575999.	2.5	39
16	Auto-ASD-Network. , 2019, , .		41
17	LBE: A Computational Load Balancing Algorithm for Speeding up Parallel Peptide Search in Mass-Spectrometry Based Proteomics. , 2019, , .		5
18	Optimized CNN-based Diagnosis System to Detect the Pneumonia from Chest Radiographs. , 2019, , .		14

#	ARTICLE	IF	CITATIONS
19	Efficient Shared Peak Counting in Database Peptide Search Using Compact Data Structure for Fragment-Ion Index. , 2019, , .		3
20	GPU-SFFT: A GPU based parallel algorithm for computing the Sparse Fast Fourier Transform (SFFT) of k-sparse signals. , 2019, , .		5
21	ASD-DiagNet: A Hybrid Learning Approach for Detection of Autism Spectrum Disorder Using fMRI Data. Frontiers in Neuroinformatics, 2019, 13, 70.	2.5	188
22	GPU-DFC: A GPU-Based Parallel Algorithm for Computing Dynamic-Functional Connectivity of Big fMRI Data. , 2019, , .		1
23	Parallel Sampling-Pipeline for Indefinite Stream of Heterogeneous Graphs using OpenCL for FPGAs. , 2018, , .		1
24	A Fourier-Based Data Minimization Algorithm for Fast and Secure Transfer of Big Genomic Datasets. , 2018, , .		1
25	Similarity based classification of ADHD using singular value decomposition. , 2018, , .		20
26	MaSSâ€”Simulator: A Highly Configurable Simulator for Generating MS/MS Datasets for Benchmarking of Proteomics Algorithms. Proteomics, 2018, 18, e1800206.	2.2	12
27	GPU-DAEMON: GPU algorithm design, data management & optimization template for array based big omics data. Computers in Biology and Medicine, 2018, 101, 163-173.	7.0	10
28	Fast-GPU-PCC: A GPU-Based Technique to Compute Pairwise Pearsonâ€™s Correlation Coefficients for Time Series Dataâ€™fMRI Study. High-Throughput, 2018, 7, 11.	4.4	18
29	Towards quantifying psychiatric diagnosis using machine learning algorithms and big fMRI data. Big Data Analytics, 2018, 3, .	2.2	11
30	A Hybrid MPI-OpenMP Strategy to Speedup the Compression of Big Next-Generation Sequencing Datasets. IEEE Transactions on Parallel and Distributed Systems, 2017, 28, 2760-2769.	5.6	11
31	A New Cryptography Algorithm to Protect Cloud-Based Healthcare Services. , 2017, , .		13
32	GPU-PCC. , 2017, , .		8
33	An Out-of-Core GPU based Dimensionality Reduction Algorithm for Big Mass Spectrometry Data and Its Application in Bottom-up Proteomics. , 2017, 2017, 550-555.		10
34	Scalable data structure to compress next-generation sequencing files and its application to compressive genomics. , 2017, , .		0
35	Power-efficient and highly scalable parallel graph sampling using FPGAs. , 2017, , .		4
36	Introduction to the selected papers from the 7th International Conference on Bioinformatics and Computational Biology (BICoB 2015). Journal of Bioinformatics and Computational Biology, 2016, 14, 1602002.	0.8	0

#	ARTICLE	IF	CITATIONS
37	GPU-ArraySort: A Parallel, In-Place Algorithm for Sorting Large Number of Arrays. , 2016, , .		6
38	A parallel peptide indexer and decoy generator for crux tide using OpenMP. , 2016, , .		3
39	Systems-level analysis reveals selective regulation of Aqp2 gene expression by vasopressin. Scientific Reports, 2016, 6, 34863.	3.3	35
40	MS-REDUCE: an ultrafast technique for reduction of big mass spectrometry data for high-throughput processing. Bioinformatics, 2016, 32, 1518-1526.	4.1	22
41	Data Aware Communication for Energy Harvesting Sensor Networks. Lecture Notes in Computer Science, 2016, , 121-132.	1.3	0
42	A Variable-Length Network Encoding Protocol for Big Genomic Data. Lecture Notes in Computer Science, 2016, , 212-224.	1.3	2
43	Big data proteogenomics and high performance computing: Challenges and opportunities. , 2015, , .		4
44	Autophagic degradation of aquaporin-2 is an early event in hypokalemia-induced nephrogenic diabetes insipidus. Scientific Reports, 2015, 5, 18311.	3.3	53
45	A Parallel Algorithm for Compression of Big Next-Generation Sequencing Datasets. , 2015, , .		1
46	Design and Implementation of Network Transfer Protocol for Big Genomic Data. , 2015, , .		7
47	Global analysis of the effects of the V2 receptor antagonist satavaptan on protein phosphorylation in collecting duct. American Journal of Physiology - Renal Physiology, 2014, 306, 410-421.	2.7	13
48	CAMS-RS: Clustering Algorithm for Large-Scale Mass Spectrometry Data Using Restricted Search Space and Intelligent Random Sampling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 128-141.	3.0	22
49	A knowledge base of vasopressin actions in the kidney. American Journal of Physiology - Renal Physiology, 2014, 307, F747-F755.	2.7	10
50	Exploiting thread-level and instruction-level parallelism to cluster mass spectrometry data using multicore architectures. Network Modeling Analysis in Health Informatics and Bioinformatics, 2014, 3, 54.	2.1	1
51	PhosSA: Fast and accurate phosphorylation site assignment algorithm for mass spectrometry data. Proteome Science, 2013, 11, S14.	1.7	10
52	A high performance algorithm for clustering of large-scale protein mass spectrometry data using multi-core architectures. , 2013, , .		2
53	Proteome-Wide Measurement of Protein Half-Lives and Translation Rates in Vasopressin-Sensitive Collecting Duct Cells. Journal of the American Society of Nephrology: JASN, 2013, 24, 1793-1805.	6.1	93
54	FOREWORD TO THE SPECIAL ISSUE ON SELECTED PAPERS FROM THE 5TH INTERNATIONAL CONFERENCE ON BIOINFORMATICS AND COMPUTATIONAL BIOLOGY (BICoB 2013). Journal of Bioinformatics and Computational Biology, 2013, 11, 1302002.	0.8	0

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55	Identifying protein kinase target preferences using mass spectrometry. American Journal of Physiology - Cell Physiology, 2012, 303, C715-C727.	4.6	58
56	Quantitative phosphoproteomics in nuclei of vasopressin-sensitive renal collecting duct cells. American Journal of Physiology - Cell Physiology, 2012, 303, C1006-C1020.	4.6	26
57	High performance <u>phos</u>phorylation <u>s</u>ite <u>a</u>ssignment algorithm for mass spectrometry data using multicore systems. , 2012, , .		2
58	NHLBI-<i>AbDesigner</i>: an online tool for design of peptide-directed antibodies. American Journal of Physiology - Cell Physiology, 2012, 302, C154-C164.	4.6	33
59	An efficient dynamic programming algorithm for phosphorylation site assignment of large-scale mass spectrometry data. , 2012, , 618-625.		13
60	Dynamics of the G Protein-coupled Vasopressin V2 Receptor Signaling Network Revealed by Quantitative Phosphoproteomics. Molecular and Cellular Proteomics, 2012, 11, M111.014613.	3.8	70
61	An efficient algorithm for clustering of large-scale mass spectrometry data. , 2012, , 1-4.		9
62	<scp>CP</scp>hos: A program to calculate and visualize evolutionarily conserved functional phosphorylation sites. Proteomics, 2012, 12, 3299-3303.	2.2	25
63	A high performance multiple sequence alignment system for pyrosequencing reads from multiple reference genomes. Journal of Parallel and Distributed Computing, 2012, 72, 83-93.	4.1	10
64	Mappingâ€based temporal pattern mining algorithm (MTPMA) identifies unique clusters of phosphopeptides regulated by vasopressin in collecting duct. FASEB Journal, 2011, 25, 921.4.	0.5	0
65	A domain decomposition strategy for alignment of multiple biological sequences on multiprocessor platforms. Journal of Parallel and Distributed Computing, 2009, 69, 666-677.	4.1	13
66	Multiple Sequence Alignment System for Pyrosequencing Reads. Lecture Notes in Computer Science, 2009, , 362-375.	1.3	6
67	Sample-Align-D: A high performance Multiple Sequence Alignment system using phylogenetic sampling and domain decomposition. Parallel and Distributed Processing Symposium (IPDPS), Proceedings of the International Conference on, 2008, , .	1.0	4