

Somali Chaterji

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

1,407
citations

623734

14
h-index

552781

26
g-index

41
all docs

41
docs citations

41
times ranked

2403
citing authors

#	ARTICLE	IF	CITATIONS
1	Lerna: transformer architectures for configuring error correction tools for short- and long-read genome sequencing. BMC Bioinformatics, 2022, 23, 25.	2.6	5
2	Hybrid Low-Power Wide-Area Mesh Network for IoT Applications. IEEE Internet of Things Journal, 2021, 8, 901-915.	8.7	54
3	Simultaneous learning of individual microRNA-gene interactions and regulatory comodules. BMC Bioinformatics, 2021, 22, 237.	2.6	1
4	Benchmarking Video Object Detection Systems on Embedded Devices under Resource Contention. , 2021, , .		8
5	Lattice: A Vision for Machine Learning, Data Engineering, and Policy Considerations for Digital Agriculture at Scale. IEEE Open Journal of the Computer Society, 2021, 2, 227-240.	7.8	12
6	A data-driven approach to increasing the lifetime of IoT sensor nodes. Scientific Reports, 2021, 11, 22459.	3.3	14
7	Vision Paper: Grand Challenges in Resilience: Autonomous System Resilience through Design and Runtime Measures. IEEE Open Journal of the Computer Society, 2020, 1, 155-172.	7.8	14
8	Combinatorial screening of biochemical and physical signals for phenotypic regulation of stem cellâ€‘based cartilage tissue engineering. Science Advances, 2020, 6, eaaz5913.	10.3	42
9	ApproxDet. , 2020, , .		23
10	JANUS: Benchmarking Commercial and Open-Source Cloud and Edge Platforms for Object and Anomaly Detection Workloads. , 2020, , .		6
11	Scalable Genome Assembly through Parallel de Bruijn Graph Construction for Multiple k-mers. Scientific Reports, 2019, 9, 14882.	3.3	8
12	AIKYATAN: mapping distal regulatory elements using convolutional learning on GPU. BMC Bioinformatics, 2019, 20, 488.	2.6	1
13	Athena: Automated Tuning of k-mer based Genomic Error Correction Algorithms using Language Models. Scientific Reports, 2019, 9, 16157.	3.3	6
14	Panel 2 Position Paper: AI could Solve the Worldâ€™s Healthcare Problems and that too at Scale!. , 2019, , .		0
15	Panel 3 Position Paper: Blockchain can be the Backbone of Indiaâ€™s Economy. , 2019, , .		1
16	MG-RAST version 4â€™lessons learned from a decade of low-budget ultra-high-throughput metagenome analysis. Briefings in Bioinformatics, 2019, 20, 1151-1159.	6.5	98
17	Federation in genomics pipelines: techniques and challenges. Briefings in Bioinformatics, 2019, 20, 235-244.	6.5	18
18	A Distributed Classifier for MicroRNA Target Prediction with Validation Through TCGA Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1037-1051.	3.0	9

#	ARTICLE	IF	CITATIONS
19	Minerva: A reinforcement learning-based technique for optimal scheduling and bottleneck detection in distributed factory operations. , 2018, , .		19
20	Syndecan-1 in mechanosensing of nanotopological cues in engineered materials. Biomaterials, 2018, 155, 13-24.	11.4	16
21	Tiresias: Context-sensitive Approach to Decipher the Presence and Strength of MicroRNA Regulatory Interactions. Theranostics, 2018, 8, 277-291.	10.0	22
22	Scalable Genomic Assembly through Parallel <i>de Bruijn</i> Graph Construction for Multiple K-mers. , 2017, , .		7
23	Suitability of NoSQL systems “ Cassandra and ScyllaDB ” For IoT workloads. , 2017, , .		5
24	Rafiki. , 2017, , .		33
25	Prediction of enhancer RNA activity levels from CHIP-seq-derived histone modification combinatorial codes. , 2017, , .		1
26	CRISPR Genome Engineering for Human Pluripotent Stem Cell Research. Theranostics, 2017, 7, 4445-4469.	10.0	22
27	EP-DNN: A Deep Neural Network-Based Global Enhancer Prediction Algorithm. Scientific Reports, 2016, 6, 38433.	3.3	42
28	SARVAVID. , 2016, , .		14
29	Fast training on large genomics data using distributed Support Vector Machines. , 2016, , .		3
30	Opening up the blackbox: an interpretable deep neural network-based classifier for cell-type specific enhancer predictions. BMC Systems Biology, 2016, 10, 54.	3.0	25
31	The MG-RAST metagenomics database and portal in 2015. Nucleic Acids Research, 2016, 44, D590-D594.	14.5	187
32	Interpretable deep neural networks for enhancer prediction. , 2015, , .		2
33	An ensemble SVM model for the accurate prediction of non-canonical MicroRNA targets. , 2015, , .		12
34	MicroRNA target prediction using thermodynamic and sequence curves. BMC Genomics, 2015, 16, 999.	2.8	28
35	Syndecan-1 Regulates Vascular Smooth Muscle Cell Phenotype. PLoS ONE, 2014, 9, e89824.	2.5	27
36	Orion: Scaling Genomic Sequence Matching with Fine-Grained Parallelization. , 2014, , .		9

#	ARTICLE	IF	CITATIONS
37	Synergistic Effects of Matrix Nanotopography and Stiffness on Vascular Smooth Muscle Cell Function. <i>Tissue Engineering - Part A</i> , 2014, 20, 2115-2126.	3.1	48
38	Scaffold-Free <i>In Vitro</i> Arterial Mimetics: The Importance of Smooth Muscle-Endothelium Contact. <i>Tissue Engineering - Part A</i> , 2010, 16, 1901-1912.	3.1	24
39	Smart polymeric gels: Redefining the limits of biomedical devices. <i>Progress in Polymer Science</i> , 2007, 32, 1083-1122.	24.7	538