

Mehmet GÃ¼ltas

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

366
citations

840776

11
h-index

888059

17
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41
all docs

41
docs citations

41
times ranked

470
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Investigation of Gene Regulatory Processes Underlying Avian Influenza Viruses in Chicken and Duck. <i>Biology</i> , 2022, 11, 219.	2.8	3
2	agReg-SNPdb-Plants: A Database of Regulatory SNPs for Agricultural Plant Species. <i>Biology</i> , 2022, 11, 684.	2.8	0
3	Deciphering the Molecular Mechanism Underlying African Animal Trypanosomiasis by Means of the 1000 Bull Genomes Project Genomic Dataset. <i>Biology</i> , 2022, 11, 742.	2.8	1
4	Deciphering Pleiotropic Signatures of Regulatory SNPs in <i>Zea mays</i> L. Using Multi-Omics Data and Machine Learning Algorithms. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5121.	4.1	2
5	In Silico Identification of the Complex Interplay between Regulatory SNPs, Transcription Factors, and Their Related Genes in <i>Brassica napus</i> L. Using Multi-Omics Data. <i>International Journal of Molecular Sciences</i> , 2021, 22, 789.	4.1	12
6	Computational Identification of Master Regulators Influencing Trypanotolerance in Cattle. <i>International Journal of Molecular Sciences</i> , 2021, 22, 562.	4.1	2
7	Unravelling the Complex Interplay of Transcription Factors Orchestrating Seed Oil Content in <i>Brassica napus</i> L. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1033.	4.1	9
8	A graph-based algorithm for detecting rigid domains in protein structures. <i>BMC Bioinformatics</i> , 2021, 22, 66.	2.6	1
9	Ultrastructural maturation of the endbulb of Held active zones comparing wild-type and otoferlin-deficient mice. <i>IScience</i> , 2021, 24, 102282.	4.1	5
10	Is There a Link between Suckling and Manipulation Behavior during Rearing in Pigs?. <i>Animals</i> , 2021, 11, 1175.	2.3	1
11	In Silico Prediction of Transcription Factor Collaborations Underlying Phenotypic Sexual Dimorphism in Zebrafish (<i>Danio rerio</i>). <i>Genes</i> , 2021, 12, 873.	2.4	0
12	agReg-SNPdb: A Database of Regulatory SNPs for Agricultural Animal Species. <i>Biology</i> , 2021, 10, 790.	2.8	6
13	MIDESP: Mutual Information-Based Detection of Epistatic SNP Pairs for Qualitative and Quantitative Phenotypes. <i>Biology</i> , 2021, 10, 921.	2.8	3
14	Detecting Animal Contacts – A Deep Learning-Based Pig Detection and Tracking Approach for the Quantification of Social Contacts. <i>Sensors</i> , 2021, 21, 7512.	3.8	17
15	Survey data to identify the selection criteria used by breeders of four strains of Pakistani beetal goats. <i>Data in Brief</i> , 2020, 32, 106051.	1.0	2
16	Genotyping by Sequencing Reads of 20 <i>Vicia faba</i> Lines with High and Low Vicine and Convicine Content. <i>Data</i> , 2020, 5, 63.	2.3	0
17	Combining Random Forests and a Signal Detection Method Leads to the Robust Detection of Genotype-Phenotype Associations. <i>Genes</i> , 2020, 11, 892.	2.4	12
18	Investigation of Pig Activity Based on Video Data and Semi-Supervised Neural Networks. <i>AgriEngineering</i> , 2020, 2, 581-595.	3.2	11

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19	Breeding objectives and selection criteria for four strains of Pakistani Beetal goats identified in a participatory approach. <i>Small Ruminant Research</i> , 2020, 190, 106163.	1.2	7
20	Identifying Cattle Breed-Specific Partner Choice of Transcription Factors during the African Trypanosomiasis Disease Progression Using Bioinformatics Analysis. <i>Vaccines</i> , 2020, 8, 246.	4.4	6
21	Identification of Regulatory SNPs Associated with Vicine and Convicine Content of <i>Vicia faba</i> Based on Genotyping by Sequencing Data Using Deep Learning. <i>Genes</i> , 2020, 11, 614.	2.4	15
22	Identification of Age-Specific and Common Key Regulatory Mechanisms Governing Eggshell Strength in Chicken Using Random Forests. <i>Genes</i> , 2020, 11, 464.	2.4	14
23	Constructing temporal regulatory cascades in the context of development and cell differentiation. <i>PLoS ONE</i> , 2020, 15, e0231326.	2.5	1
24	Genetic diversity and population structure of six ethiopian cattle breeds from different geographical regions using high density single nucleotide polymorphisms. <i>Livestock Science</i> , 2020, 234, 103979.	1.6	5
25	Computational identification of tissue-specific transcription factor cooperation in ten cattle tissues. <i>PLoS ONE</i> , 2019, 14, e0216475.	2.5	15
26	Identification of Candidate Signature Genes and Key Regulators Associated With Trypanotolerance in the Sheko Breed. <i>Frontiers in Genetics</i> , 2019, 10, 1095.	2.3	18
27	Construction and Visualization of Dynamic Biological Networks: Benchmarking the Neo4J Graph Database. <i>Lecture Notes in Computer Science</i> , 2019, , 33-43.	1.3	3
28	Big Data Technologies for DNA Sequencing. , 2019, , 330-336.		1
29	Big Data Technologies for DNA Sequencing. , 2018, , 1-6.		1
30	Removing Background Co-occurrences of Transcription Factor Binding Sites Greatly Improves the Prediction of Specific Transcription Factor Cooperations. <i>Frontiers in Genetics</i> , 2018, 9, 189.	2.3	8
31	The synaptic ribbon is critical for sound encoding at high rates and with temporal precision. <i>ELife</i> , 2018, 7, .	6.0	81
32	Computational Detection of Stage-Specific Transcription Factor Clusters during Heart Development. <i>Frontiers in Genetics</i> , 2016, 7, 33.	2.3	11
33	Computational Identification of Key Regulators in Two Different Colorectal Cancer Cell Lines. <i>Frontiers in Genetics</i> , 2016, 7, 42.	2.3	10
34	A Novel Sequence-Based Feature for the Identification of DNA-Binding Sites in Proteins Using Jensenâ€™Shannon Divergence. <i>Entropy</i> , 2016, 18, 379.	2.2	5
35	PC-TraFF: identification of potentially collaborating transcription factors using pointwise mutual information. <i>BMC Bioinformatics</i> , 2015, 16, 400.	2.6	23
36	CRF-based models of protein surfaces improve protein-protein interaction site predictions. <i>BMC Bioinformatics</i> , 2014, 15, 277.	2.6	20

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37	Quantum coupled mutation finder: predicting functionally or structurally important sites in proteins using quantum Jensen-Shannon divergence and CUDA programming. BMC Bioinformatics, 2014, 15, 96.	2.6	7
38	Coupled mutation finder: A new entropy-based method quantifying phylogenetic noise for the detection of compensatory mutations. BMC Bioinformatics, 2012, 13, 225.	2.6	8
39	The sponge genetree server—providing a phylogenetic backbone for poriferan evolutionary studies. Zootaxa, 2008, 1939, 58-60.	0.5	19