## A Ercument Cicek

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	27.8	2,254
2	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	28.9	1,422
3	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	8.1	1,219
4	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	14.8	952
5	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. American Journal of Human Genetics, 2018, 102, 1169-1184.	6.2	128
6	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489.	6.4	91
7	Metabolome Profiling by HRMAS NMR Spectroscopy of Pheochromocytomas and Paragangliomas Detects SDH Deficiency: Clinical and Pathophysiological Implications. Neoplasia, 2015, 17, 55-65.	5.3	60
8	Detailed modeling of positive selection improves detection of cancer driver genes. Nature Communications, 2019, 10, 3399.	12.8	49
9	Ensuring location diversity in privacy-preserving spatio-temporal data publishing. VLDB Journal, 2014, 23, 609-625.	4.1	45
10	Re-identification of individuals in genomic data-sharing beacons via allele inference. Bioinformatics, 2019, 35, 365-371.	4.1	37
11	Robust inference of kinase activity using functional networks. Nature Communications, 2021, 12, 1177.	12.8	36
12	AMULET: a novel read count-based method for effective multiplet detection from single nucleus ATAC-seq data. Genome Biology, 2021, 22, 252.	8.8	36
13	A Statistical Framework for Mapping Risk Genes from De Novo Mutations in Whole-Genome-Sequencing Studies. American Journal of Human Genetics, 2018, 102, 1031-1047.	6.2	26
14	Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm. Bioinformatics, 2020, 36, 3669-3679.	4.1	26
15	Hercules: a profile HMM-based hybrid error correction algorithm for long reads. Nucleic Acids Research, 2018, 46, e125.	14.5	23
16	De novo missense variants disrupting protein–protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types. Molecular Autism, 2020, 11, 76.	4.9	19
17	ADEMA: An Algorithm to Determine Expected Metabolite Level Alterations Using Mutual Information. PLoS Computational Biology, 2013, 9, e1002859.	3.2	18
18	Metabolomic characterization of human hippocampus from drugâ€resistant epilepsy with mesial temporal seizure. Epilepsia, 2018, 59, 607-616.	5.1	18

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19	Matrix Metalloproteinase-11 Promotes Early Mouse Mammary Gland Tumor Growth through Metabolic Reprogramming and Increased IGF1/AKT/FoxO1 Signaling Pathway, Enhanced ER Stress and Alteration in Mitochondrial UPR. Cancers, 2020, 12, 2357.	3.7	17
20	Genetic circuits combined with machine learning provides fast responding living sensors. Biosensors and Bioelectronics, 2021, 178, 113028.	10.1	16
21	Machine learning assisted intraoperative assessment of brain tumor margins using HRMAS NMR spectroscopy. PLoS Computational Biology, 2020, 16, e1008184.	3.2	16
22	High-resolution magic angle spinning 1H nuclear magnetic resonance spectroscopy metabolomics of hyperfunctioning parathyroid glands. Surgery, 2016, 160, 384-394.	1.9	12
23	Genome Reconstruction Attacks Against Genomic Data-Sharing Beacons. Proceedings on Privacy Enhancing Technologies, 2021, 2021, 28-48.	2.8	12
24	Metabolomics approaches in experimental allergic encephalomyelitis. Journal of Neuroimmunology, 2018, 314, 94-100.	2.3	11
25	PathCase-SB architecture and database design. BMC Systems Biology, 2011, 5, 188.	3.0	10
26	De novo ChIP-seq analysis. Genome Biology, 2015, 16, 205.	8.8	10
27	ST-Steiner: a spatio-temporal gene discovery algorithm. Bioinformatics, 2019, 35, 3433-3440.	4.1	10
28	Metabolomic Profile of Aggressive Meningiomas by Using High-Resolution Magic Angle Spinning Nuclear Magnetic Resonance. Journal of Proteome Research, 2020, 19, 292-299.	3.7	10
29	Revisiting the complex architecture of ALS in Turkey: Expanding genotypes, shared phenotypes, molecular networks, and a public variant database. Human Mutation, 2020, 41, e7-e45.	2.5	10
30	SPADIS: An Algorithm for Selecting Predictive and Diverse SNPs in GWAS. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1208-1216.	3.0	10
31	A NEW METABOLOMICS ANALYSIS TECHNIQUE: STEADY-STATE METABOLIC NETWORK DYNAMICS ANALYSIS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1240003.	0.8	9
32	An online model composition tool for system biology models. BMC Systems Biology, 2013, 7, 88.	3.0	9
33	Metabolomics of Small Intestine Neuroendocrine Tumors and Related Hepatic Metastases. Metabolites, 2019, 9, 300.	2.9	8
34	Characterization of the transcriptional and metabolic responses of pediatric high grade gliomas to mTOR-HIF-1α axis inhibition. Oncotarget, 2017, 8, 71597-71617.	1.8	8
35	OPERATIONAL VARIABLE JOB SCHEDULING WITH ELIGIBILITY CONSTRAINTS: A RANDOMIZED CONSTRAINTâ€GRAPHâ€BASED APPROACH. Technological and Economic Development of Economy, 2009, 15, 245-266.	4.6	7
36	OBSERVATION CONFLICT RESOLUTION IN STEADY-STATE METABOLIC NETWORK DYNAMICS ANALYSIS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1240004.	0.8	6

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37	PathCase-SB: integrating data sources and providing tools for systems biology research. BMC Systems Biology, 2012, 6, 67.	3.0	6
38	iPathCaseKEGG: An iPad interface for KEGG metabolic pathways. Health Information Science and Systems, 2013, 1, 4.	5.2	6
39	An integrated genomic and metabolomic approach for defining survival time in adult oligodendrogliomas patients. Metabolomics, 2019, 15, 69.	3.0	5
40	Metabolomic profiling highlights the metabolic bases of acute-on-chronic and post-hepatectomy liver failure. Hpb, 2019, 21, 1354-1361.	0.3	5
41	Polishing copy number variant calls on exome sequencing data via deep learning. Genome Research, 2022, 32, 1170-1182.	5.5	5
42	k-Shell decomposition reveals structural properties of the gene coexpression network for neurodevelopment. Turkish Journal of Biology, 2017, 41, 333-341.	0.8	4
43	The effect of kinship in re-identification attacks against genomic data sharing beacons. Bioinformatics, 2020, 36, i903-i910.	4.1	4
44	DeepND: Deep multitask learning of gene risk for comorbid neurodevelopmental disorders. Patterns, 2022, , 100524.	5.9	4
45	MIRA: mutual information-based reporter algorithm for metabolic networks. Bioinformatics, 2014, 30, i175-i184.	4.1	3
46	Predicting Carbon Spectrum in Heteronuclear Single Quantum Coherence Spectroscopy for Online Feedback During Surgery. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	3
47	Potpourri: An Epistasis Test Prioritization Algorithm via Diverse SNP Selection. Journal of Computational Biology, 2021, 28, 365-377.	1.6	3
48	Targeted metabolomics analyses for brain tumor margin assessment during surgery. Bioinformatics, 2022, 38, 3238-3244.	4.1	3
49	What Does Reduced FDG Uptake Mean in High-Grade Gliomas?. Clinical Nuclear Medicine, 2019, 44, 936-942.	1.3	2
50	A unifying network modeling approach for codon optimization. Bioinformatics, 2022, 38, 3935-3941.	4.1	2
51	DORMAN: Database of Reconstructed MetAbolic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1474-1480.	3.0	1
52	A Tool for Detecting Complementary Single Nucleotide Polymorphism Pairs in Genome-Wide Association Studies for Epistasis Testing. Journal of Computational Biology, 2021, 28, 378-380.	1.6	1
53	Uncovering complementary sets of variants for predicting quantitative phenotypes. Bioinformatics, 2022, 38, 908-917.	4.1	1
54	PathCase-MAW. , 2013, , .		0

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55	Potpourri: An Epistasis Test Prioritization Algorithm via Diverse SNP Selection. Lecture Notes in Computer Science, 2020, , 243-244.	1.3	0