

# A Ercument Cicek

## List of Publications by Year in descending order

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Version: 2024-02-01

55  
papers

6,746  
citations

566801

15  
h-index

174990

52  
g-index

65  
all docs

65  
docs citations

65  
times ranked

12022  
citing authors

#	ARTICLE	IF	CITATIONS
1	Synaptic, transcriptional and chromatin genes disrupted in autism. <i>Nature</i> , 2014, 515, 209-215.	13.7	2,254
2	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. <i>Cell</i> , 2020, 180, 568-584.e23.	13.5	1,422
3	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. <i>Neuron</i> , 2015, 87, 1215-1233.	3.8	1,219
4	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	7.1	952
5	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. <i>American Journal of Human Genetics</i> , 2018, 102, 1169-1184.	2.6	128
6	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. <i>Cell Reports</i> , 2020, 31, 107489.	2.9	91
7	Metabolome Profiling by HRMAS NMR Spectroscopy of Pheochromocytomas and Paragangliomas Detects SDH Deficiency: Clinical and Pathophysiological Implications. <i>Neoplasia</i> , 2015, 17, 55-65.	2.3	60
8	Detailed modeling of positive selection improves detection of cancer driver genes. <i>Nature Communications</i> , 2019, 10, 3399.	5.8	49
9	Ensuring location diversity in privacy-preserving spatio-temporal data publishing. <i>VLDB Journal</i> , 2014, 23, 609-625.	2.7	45
10	Re-identification of individuals in genomic data-sharing beacons via allele inference. <i>Bioinformatics</i> , 2019, 35, 365-371.	1.8	37
11	Robust inference of kinase activity using functional networks. <i>Nature Communications</i> , 2021, 12, 1177.	5.8	36
12	AMULET: a novel read count-based method for effective multiplet detection from single nucleus ATAC-seq data. <i>Genome Biology</i> , 2021, 22, 252.	3.8	36
13	A Statistical Framework for Mapping Risk Genes from De Novo Mutations in Whole-Genome-Sequencing Studies. <i>American Journal of Human Genetics</i> , 2018, 102, 1031-1047.	2.6	26
14	Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm. <i>Bioinformatics</i> , 2020, 36, 3669-3679.	1.8	26
15	Hercules: a profile HMM-based hybrid error correction algorithm for long reads. <i>Nucleic Acids Research</i> , 2018, 46, e125.	6.5	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. <i>Molecular Autism</i> , 2020, 11, 76.	2.6	19
17	ADEMA: An Algorithm to Determine Expected Metabolite Level Alterations Using Mutual Information. <i>PLoS Computational Biology</i> , 2013, 9, e1002859.	1.5	18
18	Metabolomic characterization of human hippocampus from drug-resistant epilepsy with mesial temporal seizure. <i>Epilepsia</i> , 2018, 59, 607-616.	2.6	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. <i>Cancers</i> , 2020, 12, 2357.	1.7	17
20	Genetic circuits combined with machine learning provides fast responding living sensors. <i>Biosensors and Bioelectronics</i> , 2021, 178, 113028.	5.3	16
21	Machine learning assisted intraoperative assessment of brain tumor margins using HRMAS NMR spectroscopy. <i>PLoS Computational Biology</i> , 2020, 16, e1008184.	1.5	16
22	High-resolution magic angle spinning 1H nuclear magnetic resonance spectroscopy metabolomics of hyperfunctioning parathyroid glands. <i>Surgery</i> , 2016, 160, 384-394.	1.0	12
23	Genome Reconstruction Attacks Against Genomic Data-Sharing Beacons. <i>Proceedings on Privacy Enhancing Technologies</i> , 2021, 2021, 28-48.	2.3	12
24	Metabolomics approaches in experimental allergic encephalomyelitis. <i>Journal of Neuroimmunology</i> , 2018, 314, 94-100.	1.1	11
25	PathCase-SB architecture and database design. <i>BMC Systems Biology</i> , 2011, 5, 188.	3.0	10
26	De novo ChIP-seq analysis. <i>Genome Biology</i> , 2015, 16, 205.	3.8	10
27	ST-Steiner: a spatio-temporal gene discovery algorithm. <i>Bioinformatics</i> , 2019, 35, 3433-3440.	1.8	10
28	Metabolomic Profile of Aggressive Meningiomas by Using High-Resolution Magic Angle Spinning Nuclear Magnetic Resonance. <i>Journal of Proteome Research</i> , 2020, 19, 292-299.	1.8	10
29	Revisiting the complex architecture of ALS in Turkey: Expanding genotypes, shared phenotypes, molecular networks, and a public variant database. <i>Human Mutation</i> , 2020, 41, e7-e45.	1.1	10
30	SPADIS: An Algorithm for Selecting Predictive and Diverse SNPs in GWAS. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1208-1216.	1.9	10
31	A NEW METABOLOMICS ANALYSIS TECHNIQUE: STEADY-STATE METABOLIC NETWORK DYNAMICS ANALYSIS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1240003.	0.3	9
32	An online model composition tool for system biology models. <i>BMC Systems Biology</i> , 2013, 7, 88.	3.0	9
33	Metabolomics of Small Intestine Neuroendocrine Tumors and Related Hepatic Metastases. <i>Metabolites</i> , 2019, 9, 300.	1.3	8
34	Characterization of the transcriptional and metabolic responses of pediatric high grade gliomas to mTOR-HIF-1 $\alpha$ axis inhibition. <i>Oncotarget</i> , 2017, 8, 71597-71617.	0.8	8
35	OPERATIONAL VARIABLE JOB SCHEDULING WITH ELIGIBILITY CONSTRAINTS: A RANDOMIZED CONSTRAINTâ€GRAPHâ€BASED APPROACH. <i>Technological and Economic Development of Economy</i> , 2009, 15, 245-266.	2.3	7
36	OBSERVATION CONFLICT RESOLUTION IN STEADY-STATE METABOLIC NETWORK DYNAMICS ANALYSIS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1240004.	0.3	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.	3.4	6
39	An integrated genomic and metabolomic approach for defining survival time in adult oligodendrogliomas patients. Metabolomics, 2019, 15, 69.	1.4	5
40	Metabolomic profiling highlights the metabolic bases of acute-on-chronic and post-hepatectomy liver failure. Hpb, 2019, 21, 1354-1361.	0.1	5
41	Polishing copy number variant calls on exome sequencing data via deep learning. Genome Research, 2022, 32, 1170-1182.	2.4	5
42	k-Shell decomposition reveals structural properties of the gene coexpression network for neurodevelopment. Turkish Journal of Biology, 2017, 41, 333-341.	2.1	4
43	The effect of kinship in re-identification attacks against genomic data sharing beacons. Bioinformatics, 2020, 36, i903-i910.	1.8	4
44	DeepND: Deep multitask learning of gene risk for comorbid neurodevelopmental disorders. Patterns, 2022, , 100524.	3.1	4
45	MIRA: mutual information-based reporter algorithm for metabolic networks. Bioinformatics, 2014, 30, i175-i184.	1.8	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.	1.9	3
47	Potpourri: An Epistasis Test Prioritization Algorithm via Diverse SNP Selection. Journal of Computational Biology, 2021, 28, 365-377.	0.8	3
48	Targeted metabolomics analyses for brain tumor margin assessment during surgery. Bioinformatics, 2022, 38, 3238-3244.	1.8	3
49	What Does Reduced FDG Uptake Mean in High-Grade Gliomas?. Clinical Nuclear Medicine, 2019, 44, 936-942.	0.7	2
50	A unifying network modeling approach for codon optimization. Bioinformatics, 2022, 38, 3935-3941.	1.8	2
51	DORMAN: Database of Reconstructed MetAbolic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1474-1480.	1.9	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.	0.8	1
53	Uncovering complementary sets of variants for predicting quantitative phenotypes. Bioinformatics, 2022, 38, 908-917.	1.8	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.	1.0	0