# A Ercument Cicek

List of Publications by Year
in descending order

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|---|---|---|---|
| 55 papers | 6,746 citations | 567144 15 h-index | 175177 52 g-index |
| 65 all docs | 65 docs citations | 65 times ranked | 12022 citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 1 | Uncovering complementary sets of variants for predicting quantitative phenotypes. Bioinformatics, 2022, 38, 908-917. | 1.8 | 1 |
| 2 | Targeted metabolomics analyses for brain tumor margin assessment during surgery. Bioinformatics, 2022, 38, 3238-3244. | 1.8 | 3 |
| 3 | DeepND: Deep multitask learning of gene risk for comorbid neurodevelopmental disorders. Patterns, 2022, , 100524. | 3.1 | 4 |
| 4 | Polishing copy number variant calls on exome sequencing data via deep learning. Genome Research, 2022, 32, 1170-1182. | 2.4 | 5 |
| 5 | A unifying network modeling approach for codon optimization. Bioinformatics, 2022, 38, 3935-3941. | 1.8 | 2 |
| 6 | DORMAN: Database of Reconstructed MetAbolic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1474-1480. | 1.9 | 1 |
| 7 | Potpourri: An Epistasis Test Prioritization Algorithm via Diverse SNP Selection. Journal of Computational Biology, 2021, 28, 365-377. | 0.8 | 3 |
| 8 | SPADIS: An Algorithm for Selecting Predictive and Diverse SNPs in GWAS. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1208-1216. | 1.9 | 10 |
| 9 | Robust inference of kinase activity using functional networks. Nature Communications, 2021, 12, 1177. | 5.8 | 36 |
| 10 | Genetic circuits combined with machine learning provides fast responding living sensors. Biosensors and Bioelectronics, 2021, 178, 113028. | 5.3 | 16 |
| 11 | 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 |
| 12 | Genome Reconstruction Attacks Against Genomic Data-Sharing Beacons. Proceedings on Privacy Enhancing Technologies, 2021, 2021, 28-48. | 2.3 | 12 |
| 13 | AMULET: a novel read count-based method for effective multiplet detection from single nucleus ATAC-seq data. Genome Biology, 2021, 22, 252. | 3.8 | 36 |
| 14 | Metabolomic Profile of Aggressive Meningiomas by Using High-Resolution Magic Angle Spinning Nuclear Magnetic Resonance. Journal of Proteome Research, 2020, 19, 292-299. | 1.8 | 10 |
| 15 | 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. | 2.6 | 19 |
| 16 | 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. | 1.7 | 17 |
| 17 | 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. | 1.1 | 10 |
| 18 | Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm. Bioinformatics, 2020, 36, 3669-3679. | 1.8 | 26 |

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|---|---------|-----|-----------|
| 19 | Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23. | 13.5 | 1,422 |
| 20 | Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489. | 2.9 | 91 |
| 21 | The effect of kinship in re-identification attacks against genomic data sharing beacons. Bioinformatics, 2020, 36, i903-i910. | 1.8 | 4 |
| 22 | Machine learning assisted intraoperative assessment of brain tumor margins using HRMAS NMR spectroscopy. PLoS Computational Biology, 2020, 16, e1008184. | 1.5 | 16 |
| 23 | Potpourri: An Epistasis Test Prioritization Algorithm via Diverse SNP Selection. Lecture Notes in Computer Science, 2020, , 243-244. | 1.0 | 0 |
| 24 | Re-identification of individuals in genomic data-sharing beacons via allele inference. Bioinformatics, 2019, 35, 365-371. | 1.8 | 37 |
| 25 | Detailed modeling of positive selection improves detection of cancer driver genes. Nature Communications, 2019, 10, 3399. | 5.8 | 49 |
| 26 | 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 |
| 27 | An integrated genomic and metabolomic approach for defining survival time in adult oligodendrogliomas patients. Metabolomics, 2019, 15, 69. | 1.4 | 5 |
| 28 | Metabolomic profiling highlights the metabolic bases of acute-on-chronic and post-hepatectomy liver failure. Hpb, 2019, 21, 1354-1361. | 0.1 | 5 |
| 29 | ST-Steiner: a spatio-temporal gene discovery algorithm. Bioinformatics, 2019, 35, 3433-3440. | 1.8 | 10 |
| 30 | Metabolomics of Small Intestine Neuroendocrine Tumors and Related Hepatic Metastases. Metabolites, 2019, 9, 300. | 1.3 | 8 |
| 31 | What Does Reduced FDG Uptake Mean in High-Grade Gliomas?. Clinical Nuclear Medicine, 2019, 44, 936-942. | 0.7 | 2 |
| 32 | Metabolomic characterization of human hippocampus from drug‐resistant epilepsy with mesial temporal seizure. Epilepsia, 2018, 59, 607-616. | 2.6 | 18 |
| 33 | Metabolomics approaches in experimental allergic encephalomyelitis. Journal of Neuroimmunology, 2018, 314, 94-100. | 1.1 | 11 |
| 34 | Hercules: a profile HMM-based hybrid error correction algorithm for long reads. Nucleic Acids Research, 2018, 46, e125. | 6.5 | 23 |
| 35 | Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. American Journal of Human Genetics, 2018, 102, 1169-1184. | 2.6 | 128 |
| 36 | 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. | 2.6 | 26 |

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|---|---------|-----|-----------|
| 37 | k-Shell decomposition reveals structural properties of the gene coexpression network for neurodevelopment. Turkish Journal of Biology, 2017, 41, 333-341. | 2.1 | 4 |
| 38 | Characterization of the transcriptional and metabolic responses of pediatric high grade gliomas to mTOR-HIF-1Î± axis inhibition. Oncotarget, 2017, 8, 71597-71617. | 0.8 | 8 |
| 39 | Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453. | 7.1 | 952 |
| 40 | High-resolution magic angle spinning 1H nuclear magnetic resonance spectroscopy metabolomics of hyperfunctioning parathyroid glands. Surgery, 2016, 160, 384-394. | 1.0 | 12 |
| 41 | De novo ChIP-seq analysis. Genome Biology, 2015, 16, 205. | 3.8 | 10 |
| 42 | Metabolome Profiling by HRMAS NMR Spectroscopy of Pheochromocytomas and Paragangliomas Detects SDH Deficiency: Clinical and Pathophysiological Implications. Neoplasia, 2015, 17, 55-65. | 2.3 | 60 |
| 43 | Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233. | 3.8 | 1,219 |
| 44 | MIRA: mutual information-based reporter algorithm for metabolic networks. Bioinformatics, 2014, 30, i175-i184. | 1.8 | 3 |
| 45 | Ensuring location diversity in privacy-preserving spatio-temporal data publishing. VLDB Journal, 2014, 23, 609-625. | 2.7 | 45 |
| 46 | Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215. | 13.7 | 2,254 |
| 47 | An online model composition tool for system biology models. BMC Systems Biology, 2013, 7, 88. | 3.0 | 9 |
| 48 | iPathCaseKEGG: An iPad interface for KEGG metabolic pathways. Health Information Science and Systems, 2013, 1, 4. | 3.4 | 6 |
| 49 | PathCase-MAW. , 2013, , . | | 0 |
| 50 | ADEMA: An Algorithm to Determine Expected Metabolite Level Alterations Using Mutual Information. PLoS Computational Biology, 2013, 9, e1002859. | 1.5 | 18 |
| 51 | A NEW METABOLOMICS ANALYSIS TECHNIQUE: STEADY-STATE METABOLIC NETWORK DYNAMICS ANALYSIS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1240003. | 0.3 | 9 |
| 52 | OBSERVATION CONFLICT RESOLUTION IN STEADY-STATE METABOLIC NETWORK DYNAMICS ANALYSIS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1240004. | 0.3 | 6 |
| 53 | PathCase-SB: integrating data sources and providing tools for systems biology research. BMC Systems Biology, 2012, 6, 67. | 3.0 | 6 |
| 54 | PathCase-SB architecture and database design. BMC Systems Biology, 2011, 5, 188. | 3.0 | 10 |

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|---|---------|----|-----------| 
| 55 | OPERATIONAL VARIABLE JOB SCHEDULING WITH ELIGIBILITY CONSTRAINTS: A RANDOMIZED CONSTRAINTâ€GRAPHâ€BASED APPROACH. Technological and Economic Development of Economy, 2009, 15, 245-266. | 2.3 | 7 |