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Eğitim Bilgileri

- I. Doktora, Ohio State University, Moleküler, Hücresel ve Gelişim Biyolojisi Programı, Amerika Birleşik Devletleri 2000 - 2007
- II. Lisans, İhsan Doğramacı Bilkent Üniversitesi, Fen Fakültesi, Moleküler Biyoloji Ve Genetik Bölümü, Türkiye 1996 - 2000

Yabancı Diller

- I. İngilizce, C1 İleri

Yönetilen Tezler

- I. Yılmaz A., Preimplantation genetic diagnosis in balanced rearrangement carriers and investigation of inter chromosomal effect, Doktora, Ç.OĞUR(Öğrenci), 2023
- II. Yılmaz A., Gen ifadesi verilerinden derin öğrenme yaklaşımıyla genler arası dolaylı etkileşimlerin ortaya çıkarılması, Yüksek Lisans, G.ÇELEN(Öğrenci), 2022
- III. Yılmaz A., Dokuya Özgü Halkasal RNA'lar ve Kaynak Genlerinin İfade Profillerinin Araştırılması, Yüksek Lisans, E.İREM(Öğrenci), 2022
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- V. Yılmaz A., Meme Kanseri Yeni Nesil Dizileme Verilerinden Gen İfadesi ile mikroRNA ifadesi Arasındaki Karşılıklı Etkileşimin Analizi, Yüksek Lisans, S.ARI(Öğrenci), 2018
- VI. Yılmaz A., Analysis of biochemical pathway with graph based algorithms, Yüksek Lisans, E.RAVZA(Öğrenci), 2018
- VII. Yılmaz A., Analysis of Intra-tumoral Heterogeneity in Context of Tissue Specific Gene Expression with Computational Approach, Yüksek Lisans, H.BÜŞRA(Öğrenci), 2018
- VIII. YILMAZ A., İnsan Nöroblastoma Hücrelerinde Metal Uyarıcılı Oksidatif Stresle İndüklenen Alzheimer Modeli, Yüksek Lisans, E.KARAMAN(Öğrenci), 2017

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- III. **Comparative analysis of retrosynthesis applications for predicting of pathways for plant Secondary metabolite production**
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- IV. **Biofabrication of Acer palmatum-Mediated Multifunctional CuO Nanoparticles for Dye Removal, Antibacterial-Antifungal Activity, and Molecular Docking**
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- V. **PGT for structural chromosomal rearrangements in 300 couples reveals specific risk factors but an interchromosomal effect is unlikely**
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- VI. **Effect of SARS-CoV-2 infection on host competing endogenous RNA and miRNA network.**
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- VII. **Network based multifactorial modelling of miRNA-target interactions**
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- VIII. **Important biological information uncovered in previously unaligned reads from chromatin immunoprecipitation experiments (ChIP-Seq)**
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- IX. **Molecular basis for the action of a dietary flavonoid revealed by the comprehensive identification of apigenin human targets**
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- X. **Unraveling the KNOTTED1 regulatory network in maize meristems**
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- XI. **A Genome-Wide Regulatory Framework Identifies Maize Pericarp Color1 Controlled Genes**
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- XII. **Thriving under Stress: Selective Translation of HIV-1 Structural Protein mRNA during Vpr-Mediated Impairment of eIF4E Translation Activity**
Sharma A., Yilmaz A., Marsh K., Cochrane A., Boris-Lawrie K.
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- XIII. **AGRIS: the Arabidopsis Gene Regulatory Information Server, an update**
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- XIV. **Genome sequencing and analysis of the model grass Brachypodium distachyon**
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- NATURE, cilt.463, sa.7282, ss.763-768, 2010 (SCI-Expanded)
- XV. **Components and Mechanisms of Regulation of Gene Expression**
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- XVI. **The word landscape of the non-coding segments of the Arabidopsis thaliana genome**
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- XVII. **GRASSIUS: A Platform for Comparative Regulatory Genomics across the Grasses**
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- XVIII. **NOD/SCID mouse model of canine T-cell lymphoma with humoral hypercalcaemia of malignancy: cytokine gene expression profiling and in vivo bioluminescent imaging**
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- XIX. **RNA helicase A interacts with divergent lymphotropic retroviruses and promotes translation of human T-cell leukemia virus type 1**
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- XXI. **Coordinate enhancement of transgene transcription and translation in a lentiviral vector**
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- I. **Balıkesir/Antandros Antik Kenti Kazısı Toprak Örneklerinin Metagenomik Analizi**
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- II. **Convolutional Neural Network Approach to Predict Tumor Samples Using Gene Expression Data**
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- III. **Assessment of Mutation Susceptibility in DNA Sequences with Word Vectors**
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- IV. **POPcorn: An Online resource providing access to distributed and diverse maize project data**
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- I. **A New Network-Based Tool to Analyse Competing Endogenous RNAs**
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- II. **Constructing Accurate Compound Networks for Reliable Network Analysis**
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- III. **Reduction of Depression Symptoms via the Metabolites of Gut Microbiota**
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- IV. **Automation of Genetic Screening and Reporting with Snakemake**
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- V. **Prediction of Mutation Susceptibility Based on Solely DNA Sequences with Word2Vec**
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- VI. **Breast cancer gene expression profile analysis in terms of genes specific to non- breast tissues**
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- VII. **Batch Analysis of RNA-Seq Data with Docker in AWS Cloud**
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- VIII. **What is the relationship between cancer DEGs and tissue specific genes**
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- IX. **Kanserde İfadesi Değişen Genlerin Metabolit Ağı Açısından Değerlendirilmesi**
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1.Temel Onkoloji Sempozyumu, İzmir, Türkiye, 9 - 11 Mayıs 2018, ss.30
- X. **Kanser Teşhisinde Derin Öğrenme ile Sınıflandırma**
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1.Temel Onkoloji Sempozyumu, İzmir, Türkiye, 9 - 11 Mayıs 2018, ss.48
- XI. **Pinpointing the importance of compounds in human metabolic network**
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- XII. **Multifactorial Modelling of MicroRNA Associated Repression and Its Subsequent Effects on Gene Expression in MicroRNA:Target Network**
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- XIII. **RIGOROUS IDENTIFICATION OF TISSUE SPECIFIC GENES IN SILICO: REVEALING THE INTERPLAY BETWEEN CANCER SPECIFIC EXPRESSION AND TISSUE SPECIFIC EXPRESSION**
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- XIV. **GENERATING LOSSLESS COMPRESSION OF GENOME SCALE K-MER FREQUENCY TABLE AS RASTER IMAGE**
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- XV. **IDENTIFICATION of TISSUE SPECIFIC GENES and ASSESMENT of THEIR INTERSECTION WITH DIFFERENTIALY EXPRESSED GENES in CANCER DATA to UNDERSTAND TUMOR HETEROGENEITY IN**

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- XVI. **SURVEY OF CHIMERIC mRNAs IN HIV INFECTED PATIENT RNA-SEQ DATA**
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- XVII. **Prebiotics and Probiotics: Break the 'Self-Domino Effect' for obesity Treatment**
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- XVIII. **Robust and Rigorous Classification of Tissue Specific Genes**
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- XIX. **Prediction of splice site using AdaBoost with a new sequence encoding approach**
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- XX. **A Combined SVM and Markov Model approach for Splice Site Identification**
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- XXI. **A Novel Method for Splice Sites Prediction Using Sequence Component and Hidden Markov Model**
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- XXII. **Utilization of Multiple Mapped Sequences in Next Generation Sequencing Especially in Chip Seq Experiments**
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- XXIII. **Computational Identification of miRNA Targets Using Olive Library**
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- XXIV. **Molecular Analysis of Lipid Transfer Gene Selected from Olive Olea europaea ESTs Expressed Sequence Tags Collection**
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- XXV. **Construction and Comparison of EST Library for Expressed Genes in Normal and Tumoral Mammary Gland Tissue of the Terrier Dog**
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- XXVI. **Design and synthesis of small peptide sequences to detect concentrations of free transition metal ions**
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- XXVII. **Analyses of EST Collection from Prenatal and Postnatal Mammary Tissue of Sheep**
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- XXVIII. **Discovery of regulatory networks in plants by linking promoter and transcription factor databases.**
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- XXIX. **Construction of genomic regulatory encyclopedias: Strategies and case studies**
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Desteklenen Projeler

- I. Çakır R., Yılmaz A., Çalık H., Arı Yuka S., Maden H., TÜSEB A Grubu Acil AR-GE Projesi, Kolorektal Kanserde Çoklu İlaç Direncine Karşı In Siliko Terapötik Peptit Tasarlanması ve Kitosan Nanopartikülleri ile Etkinliğinin In Vitro İncelenmesi, 2024 - 2026
- II. YILMAZ A., Yükseköğretim Kurumları Destekli Proje, İnsan Nöroblastoma Hücrelerinde Metal-Uyarıcı Oksidatif Stresle İndüklenen Alzheimer Modeli, 2016 - 2017
- III. YILMAZ A., BULUT YILGÖR M., ÖZTAŞ E. S., TÜBİTAK Projesi, Bazı Sonlu Halkalar Üzerinde Tanımlı Ters Sıralı-Tamlama Kodlar Ve DNA\'ya Uygulamaları, 2013 - 2015