Prof.Dr. TUNCA DOĞAN

Kişisel Bilgiler

İş Telefonu: +90 312 297 7193 Dahili: 115
E-posta: tuncadogan@hacettepe.edu.tr
Web: https://yunus.hacettepe.edu.tr/~tuncadogan/
Posta Adresi: Hacettepe Üniversitesi Beytepe Yerleşkesi, Bilgisayar Mühendisliği Bölümü, kat:2 ofis no: 210, Çankaya, 06800 Ankara

Uluslararası Araştırmacı ID'leri
ScholarID: tHnMNPEAAAAJ
ORCID: 0000-0002-1298-9763
Publons / Web Of Science ResearcherID: B-5274-2017
ScopusID: 56940345200
Yoksis Araştırmacı ID: 130530

Araştırma Alanları

Biyoenformatik, Biyohesaplama , Yapay Zeka, Bilgisayarda Öğrenme ve Örüntü Tanıma, Bilgisayar Öğrenimi, Sinirsel Ağlar , Biyokimya, Proteomiks, Yapısal Biyoloji, Biyoinformatik, Biyoenformasyon, Biyolojik Modelleme, Biyolojik Veritabanları

Akademik Unvanlar / Görevler

Prof.Dr., Hacettepe Üniversitesi, Mühendislik Fakültesi, Bilgisayar Mühendisliği Bölümü, 2023 - Devam Ediyor
Doç.Dr., Hacettepe Üniversitesi, Mühendislik Fakültesi, Bilgisayar Mühendisliği Bölümü, 2021 - 2023
Dr.Öğr.Üyesi, Hacettepe Üniversitesi, Mühendislik Fakültesi, Bilgisayar Mühendisliği Bölümü, 2019 - 2021
Dr.Öğr.Üyesi, Hacettepe Üniversitesi, Bilişim Enstitüsü, Sağlık Bilişimi A.B.D., 2019 - 2021
Öğretim Görevlisi Dr., Orta Doğu Teknik Üniversitesi, Enformatik Enstitüsü, Sağlık Bilişimi Anabilim Dalı, 2016 - 2019
Öğretim Görevlisi Dr., University of Cambridge, 2013 - 2016
Araştırma Görevlisi, İzmir Yüksek Teknoloji Enstitüsü, Mühendislik Fakültesi, Elektrik-Elektronik Mühendisliği Bölümü, 2008 - 2013
Araştırma Görevlisi, Orta Doğu Teknik Üniversitesi, Mühendislik Fakültesi, Gıda Mühendisliği Bölümü, 2005 - 2008

Akademik İdari Deneyim

Anabilim/Bilim Dalı Başkanı, Hacettepe Üniversitesi, Bilişim Enstitüsü, Sağlık Bilişimi A.B.D., 2021 - Devam Ediyor

SCI, SSCI ve AHCI İndekslerine Giren Dergilerde Yayınlanan Makaleler

I. **An integrative framework for clinical diagnosis and knowledge discovery from exome sequencing data**
Shojaei M., Mohammadvand N., DOĞAN T., Alkan C., Çetin Atalay R., ACAR A.
Computers in Biology and Medicine, cilt.169, 2024 (SCI-Expanded)
II. **How to approach machine learning-based prediction of drug/compound–target interactions**

Atas Guvenilir H., DOĞAN T.
Journal of Cheminformatics, cilt.15, sa.1, 2023 (SCI-Expanded)

III. **Democratizing knowledge representation with BioCypher**
Lobentanzer S., Aloy P., Baumbach J., Bohar B., Carey V. J., Charoentong P., Danhauser K., DOĞAN T., Dreo J., Dunham I., et al.
Nature Biotechnology, cilt.41, sa.8, ss.1056-1059, 2023 (SCI-Expanded)

IV. **SELFormer: molecular representation learning via SELFIES language models**
Yüksel A., Ulusoy E., Ünlü A., DOĞAN T.
Machine Learning: Science and Technology, cilt.4, sa.2, 2023 (SCI-Expanded)

V. **ProFAB-open protein functional annotation benchmark**
Özdilek A. S., ATAKAN A., ÖZSARI G., Acar A., ATALAY M. V., DOĞAN T., Rifaioğlu A. S.
Briefings in bioinformatics, cilt.24, sa.2, 2023 (SCI-Expanded)

VI. **UniProt: the Universal Protein Knowledgebase in 2023**
Bateman A., Martin M., Orchard S., Magrane M., Ahmad S., Alpi E., Bowler-Barnett E. H., Britto R., Bye-A-Jee H., Cukura A., et al.
Nucleic Acids Research, cilt.51, sa.D1, 2023 (SCI-Expanded)

VII. **ASCARIS: Positional feature annotation and protein structure-based representation of single amino acid variations**
Cankara F., DOĞAN T.
Computational and Structural Biotechnology Journal, cilt.21, ss.4743-4758, 2023 (SCI-Expanded)

VIII. **SLPred: a multi-view subcellular localization prediction tool for multi-location human proteins**
ÖZSARI G., RİFAİOĞLU A. S., ATAKAN A., Tunca Dogan T., Martin M. J., ATALAY R., ATALAY M. V.
BIOINFORMATICS, cilt.38, sa.17, ss.4226-4229, 2022 (SCI-Expanded)

IX. **Learning functional properties of proteins with language models**
Unsal S., Atas H., Albayrak M., Turhan K., Acar A. C., Doğan T.
NATURE MACHINE INTELLIGENCE, cilt.4, sa.3, ss.227-245, 2022 (SCI-Expanded)

X. **Machine learning-based prediction of drug approvals using molecular, physicochemical, clinical trial, and patent-related features**
Ciray F., DOĞAN T.
Expert Opinion on Drug Discovery, cilt.17, sa.12, ss.1425-1441, 2022 (SCI-Expanded)

XI. **A crowdsourcing open platform for literature curation in UniProt**
Wang Y., Wang Q., Huang H., Huang W., Chen Y., McGarvey P. B., Wu C. H., Arighi C. N.
PLOS BIOLOGY, cilt.19, sa.12, 2021 (SCI-Expanded)

XII. **Editorial: Machine Learning Methodologies to Study Molecular Interactions**
Yakimovich A., oezguer A., DOĞAN T., Ozkirimli E.
FRONTIERS IN MOLECULAR BIOSCIENCES, cilt.8, 2021 (SCI-Expanded)

XIII. **Protein domain-based prediction of drug/compound-target interactions and experimental validation on LIM kinases**
Doğan T., Guzelcan E. A., Baumann M., Koyas A., Atas H., Baxendale I., Martin M., Cetin-Atalay R.
PLOS COMPUTATIONAL BIOLOGY, cilt.17, sa.11, 2021 (SCI-Expanded)

XIV. **CROssBAR: comprehensive resource of biomedical relations with knowledge graph representations**
Doğan T., Atas H., Joshi V., Atakan A., Rifaioğlu A. S., Nalbat E., Nightingale A., Saidi R., Volynkin V., Zellner H., et al.
NUCLEIC ACIDS RESEARCH, cilt.49, sa.16, 2021 (SCI-Expanded)

XV. **Crowdsourced mapping of unexplored target space of kinase inhibitors**
Cichonska A., Ravikumar B., Allaway R. J., Wan F., Park S., Isayev O., Li S., Mason M., Lamb A., Tanoli Z., et al.
NATURE COMMUNICATIONS, cilt.12, sa.1, 2021 (SCI-Expanded)

XVI. **MDeePred: novel multi-channel protein featurization for deep learning-based binding affinity prediction in drug discovery**
Rifaioglu A. S., Atalay R. C., KAHRAMAN D. C., DOĞAN T., Martin M., Atalay V.
BIOINFORMATICS, cilt.37, sa.5, ss.693-704, 2021 (SCI-Expanded)

XVII. **UniProt: the universal protein knowledgebase in 2021**

Bateman A., Martin M., Orchard S., Magrane M., Agivetova R., Ahmad S., Alpi E., Bowler-Barnett E. H., Britto R., Bursteinas B., et al.
NUCLEIC ACIDS RESEARCH, cilt.49, sa.D1, 2021 (SCI-Expanded)

XVIII. **iBioProVis: interactive visualization and analysis of compound bioactivity space**
DÖNMEZ A., RİFAİOĞLU A. S., ACAR A. C., DOĞAN T., ATALAY R., ATALAY M. V.
BIOINFORMATICS, cilt.36, sa.14, ss.4227-4230, 2020 (SCI-Expanded)

XIX. **DEEPScreen: high performance drug-target interaction prediction with convolutional neural networks using 2-D structural compound representations**
Rifaioğlu A. S., Nalbat E., Atalay V., Martin M. J., Cetin-Atalay R., Doğan T.
CHEMICAL SCIENCE, cilt.11, sa.9, ss.2531-2557, 2020 (SCI-Expanded)

XX. **The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens**
Zhou N., Jiang Y., Bergquist T. R., Lee A. J., Kacsoh B. Z., Crocker A. W., Lewis K. A., Georghiou G., Nguyen H. N., Hamid M. N., et al.
GENOME BIOLOGY, cilt.20, sa.1, 2019 (SCI-Expanded)

XXI. **FAIR adoption, assessment and challenges at UniProt**
Garcia L., Bolleman J., Gehant S., Redaschi N., Martin M., Bateman A., Magrane M., Martin M., Orchard S., Raj S., et al.
SCIENTIFIC DATA, cilt.6, 2019 (SCI-Expanded)

XXII. **Recent applications of deep learning and machine intelligence on in silico drug discovery: methods, tools and databases**
Rifaioğlu A. S., Atas H., Martin M. J., Cetin-Atalay R., Atalay V., Dogan T.
BRIEFINGS IN BIOINFORMATICS, cilt.20, sa.5, ss.1878-1912, 2019 (SCI-Expanded)

XXIII. **DEEPred: Automated Protein Function Prediction with Multi-task Feed-forward Deep Neural Networks**
Rifaioğlu A. S., Doğan T., Martin M. J., Cetin-Atalay R., Atalay V.
SCIENTIFIC REPORTS, cilt.9, 2019 (SCI-Expanded)

XXIV. **UniProt: a worldwide hub of protein knowledge**
Bateman A., Martin M., Orchard S., Magrane M., Alpi E., Bely B., Bingley M., Britto R., Bursteinas B., Busiello G., et al.
NUCLEIC ACIDS RESEARCH, cilt.47, 2019 (SCI-Expanded)

XXV. **ECPred: a tool for the prediction of the enzymatic functions of protein sequences based on the EC nomenclature**
Dalkiran A., Rifaioğlu A. S., Martin M. J., Cetin-Atalay R., Atalay V., Dogan T.
BMC BIOINFORMATICS, cilt.19, 2018 (SCI-Expanded)

XXVI. **HPO2GO: prediction of human phenotype ontology term associations for proteins using cross ontology annotation co-occurrences**
Doğan T.
PEERJ, cilt.6, 2018 (SCI-Expanded)

XXVII. **Large-scale automated function prediction of protein sequences and an experimental case study validation on PTEN transcript variants**
Rifaioğlu A. S., Dogan T., Sarac O. S., Ersahin T., Saidi R., Atalay M. V., Martin M. J., Cetin-Atalay R.
PROTEINS-STRUCTURE FUNCTION AND BIOINFORMATICS, cilt.86, sa.2, ss.135-151, 2018 (SCI-Expanded)

XXVIII. **Phylogenetic and Other Conservation-Based Approaches to Predict Protein Functional Sites**
Atas H., Tunçbağ N., Doğan T.
COMPUTATIONAL DRUG DISCOVERY AND DESIGN, cilt.1762, ss.51-69, 2018 (SCI-Expanded)

XXIX. **A Structural Perspective on the Modulation of Protein-protein Interactions with Small Molecules**
Demirel H. C., Dogan T., TUNÇBAĞ N.
CURRENT TOPICS IN MEDICINAL CHEMISTRY, cilt.18, sa.8, ss.700-713, 2018 (SCI-Expanded)

XXX. **On expert curation and scalability: UniProtKB/Swiss-Prot as a case study**
Poux S., Arighi C. N., Magrane M., Bateman A., Wei C., Lu Z., Boutet E., Bye-A-Jee H., Famiglietti M. L., Roechert B., et al.
BIOINFORMATICS, cilt.33, sa.21, ss.3454-3460, 2017 (SCI-Expanded)

XXXI. **From the research laboratory to the database: the Caenorhabditis elegans kinome in UniProtKB**
Zaru R., Magrane M., O'Donovan C., Bateman A., Martin M. J., Alpi E., Antunes R., Bely B., Bingley M., Bonilla C., et al.
BIOCHEMICAL JOURNAL, cilt.474, ss.493-515, 2017 (SCI-Expanded)

XXXII. **UniProt: the universal protein knowledgebase**
Bateman A., Martin M. J., O'Donovan C., Magrane M., Alpi E., Antunes R., Bely B., Bingley M., Bonilla C., Britto R., et al.
NUCLEIC ACIDS RESEARCH, cilt.45, 2017 (SCI-Expanded)

XXXIII. **An expanded evaluation of protein function prediction methods shows an improvement in accuracy**
Jiang Y., Oron T. R., Clark W. T., Bankapur A. R., D'Andrea D., Lepore R., Funk C. S., Kahanda I., Verspoor K. M., Ben-Hur A., et al.
GENOME BIOLOGY, cilt.17, 2016 (SCI-Expanded)

XXXIV. **UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB**
Doğan T., Macdougall A., Saidi R., Poggioli D., Bateman A., O'donovan C., Martin M. J.
BIOINFORMATICS, cilt.32, sa.15, ss.2264-2271, 2016 (SCI-Expanded)

XXXV. **The UniProtKB guide to the human proteome**
Breuza L., Poux S., Estreicher A., Famiglietti M. L., Magrane M., Tognolli M., Bridge A., Baratin D., Redaschi N., Xenarios I., et al.
DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION, 2016 (SCI-Expanded)

XXXVI. **Tools and data services registry: a community effort to document bioinformatics resources**
Ison J., Rapacki K., Menager H., Kalas M., Rydza E., Chmura P., Anthon C., Beard N., Berka K., Bolser D., et al.
NUCLEIC ACIDS RESEARCH, cilt.44, 2016 (SCI-Expanded)

XXXVII. **UniProt: a hub for protein information**
Bateman A., Martin M. J., O'Donovan C., Magrane M., Apweiler R., Alpi E., Antunes R., Arganiska J., Bely B., Bingley M., et al.
NUCLEIC ACIDS RESEARCH, cilt.43, 2015 (SCI-Expanded)

XXXVIII. **Activities at the Universal Protein Resource (UniProt)**
Apweiler R., Bateman A., Martin M. J., O'Donovan C., Magrane M., Alam-Faruque Y., Alpi E., Antunes R., Arganiska J., Casanova E. B., et al.
NUCLEIC ACIDS RESEARCH, cilt.42, 2014 (SCI-Expanded)

XXXIX. **Automatic Identification of Highly Conserved Family Regions and Relationships in Genome Wide Datasets Including Remote Protein Sequences**
Doğan T., Karacali B.
PLOS ONE, cilt.8, sa.9, 2013 (SCI-Expanded)

Diğer Dergilerde Yayınlanan Makaleler

I. **Transfer learning for drug-target interaction prediction**
DALKIRAN A., ATAKAN A., Rifaioğlu A. S., Martin M. J., Atalay R. Ç., ACAR A., DOĞAN T., ATALAY M. V.
Bioinformatics (Oxford, England), cilt.39, sa.39, 2023 (Scopus)

II. **Data Centric Molecular Analysis and Evaluation of Hepatocellular Carcinoma Therapeutics Using Machine Intelligence-Based Tools**
Cetin-Atalay R., Kahraman D. C., Nalbat E., Rifaioğlu A. S., Atakan A., Dönmez A., Atas H., Atalay M. V., Acar A. C., Doğan T.
JOURNAL OF GASTROINTESTINAL CANCER, cilt.52, sa.4, ss.1266-1276, 2021 (Hakemli Dergi)

Hakemli Kongre / Sempozyum Bildiri Kitaplarında Yer Alan Yayınlar

I. **In vitro validation of drug-target interactions revealed in silico by Comprehensive Resource of Biomedical Relations with Network Representations and Deep Learning (CROssBAR) in HCC**

NALBAT E., Rifaioglu A. S., DOĞAN T., Martin M. J., Cetin-Atalay R., ATALAY M. V.
AACR Annual Meeting, ELECTR NETWORK, 22 - 24 Haziran 2020, cilt.80

II. **Unsupervised identification of redundant domain entries in InterPro database using clustering techniques**
RİFAİOĞLU A. S., Doğan T., CAN T.
6th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics, BCB 2015, Georgia, Amerika Birleşik Devletleri, 9 - 12 Eylül 2015, ss.505-506

III. **2-D thresholding of the connectivity map following the multiple sequence alignments of diverse datasets**
Doğan T., Karaçali B.
10th IASTED International Conference on Biomedical Engineering, BioMed 2013, Innsbruck, Avusturya, 13 - 15 Şubat 2013, ss.1-8

IV. **Evolutionary relationships between gene sequences via nonlinear embedding Doğrusal olmayan gömme teknikleri altinda gen dizilerinin evrimsel ilişkileri**
Doğan T., Karaçcali B.
2010 15th National Biomedical Engineering Meeting, BIYOMUT2010, Antalya, Türkiye, 21 - 24 Nisan 2010

Desteklenen Projeler

Doğan T., TÜBİTAK Projesi, Üretken Derin Öğrenme ile Yeni Protein Dizilerinin Moleküler İşlev Odaklı Otomatik Tasarımı, 2022 - 2025
Doğan T., TÜBİTAK Projesi, Biyomoleküler ve Biyomedikal Veri İçerisindeki Kompleks ve Heterojen İlişkilerin Bütünleyici Temsili ve Derin Çizge Öğrenme Bazlı Tahmini, 2021 - 2024
Doğan T., TÜBİTAK Projesi, Çekişmeli Çizge Üretici Derin Sinir Ağları ile Hastalık Hedefli Yeni İlaç Adayı Moleküllerin De Novo Tasarımı, 2021 - 2024
DOĞAN T., Derin Öğrenme Bazlı Farmakogenomik Modelleme ile Geniş Çaplı Kanser Hücre Hattı İlaç Yanıt Tahmini, 2020 - 2022
Doğan T., Newton Programı Destekli Proje, Derin Öğrenme Teknikleri Ve Ağ Analizi Yöntemleriyle Hazırlanmış Kapsamlı Biyomedikal İlişkiler Kaynağı, 2017 - 2020
Doğan T., Diğer Uluslararası Fon Programları, Development of computational pipelines for drug discovery and repurposing, 2014 - 2018
Doğan T., Diğer Uluslararası Fon Programları, Novel computational approaches for functional annotation of large data sets of proteins, 2013 - 2015

Metrikler

Yayın: 46
Atıf (WoS): 14566
Atıf (Scopus): 19446
H-İndeks (WoS): 21
H-İndeks (Scopus): 21