Prof. TUNCA DOĞAN

Personal Information

Office Phone: +90 312 297 7193 Extension: 115
Email: tuncadogan@hacettepe.edu.tr
Web: https://yunus.hacettepe.edu.tr/~tuncadogan/
Address: Hacettepe Üniversitesi Beytepe Yerleşkesi, Bilgisayar Mühendisliği Bölümü, kat:2 ofis no: 210, Çankaya, 06800 Ankara

International Researcher IDs
ScholarID: tHnMNPEAAAAJ
ORCID: 0000-0002-1298-9763
Publons / Web Of Science ResearcherID: B-5274-2017
ScopusID: 56940345200
Yoksis Researcher ID: 130530

Research Areas

bioinformatics, Biocomputing, Artificial Intelligence, Computer Learning and Pattern Recognition, Computer Learning, Neural Networks, Biochemistry, Proteomics, Structural Biology, Bioinformatics, Biological Information, Biological Modelling, Biological Databases

Academic Titles / Tasks

Professor, Hacettepe University, Mühendislik Fakültesi, Bilgisayar Mühendisliği Bölümü, 2023 - Continues
Associate Professor, Hacettepe University, Mühendislik Fakültesi, Bilgisayar Mühendisliği Bölümü, 2021 - 2023
Assistant Professor, Hacettepe University, Mühendislik Fakültesi, Bilgisayar Mühendisliği Bölümü, 2019 - 2021
Assistant Professor, Hacettepe University, Bilişim Enstitüsü, Sağlık Bilişimi A.B.D., 2019 - 2021
Lecturer PhD, Middle East Technical University, Graduate School Of Informatics, Medical Informatics, 2016 - 2019
Lecturer PhD, University of Cambridge, 2013 - 2016
Research Assistant, Izmir Institute Of Technology, Faculty Of Engıneerıng, Department Of Electrıcal And Electronıcs Engıneerıng, 2008 - 2013
Research Assistant, Middle East Technical University, Faculty Of Engineering, Department Of Food Engineering, 2005 - 2008

Academic and Administrative Experience

Head of Department, Hacettepe University, Bilişim Enstitüsü, Sağlık Bilişimi A.B.D., 2021 - Continues

Published journal articles indexed by SCI, SSCI, and AHCI

I. **Design, synthesis, and evaluation of novel Indole-Based small molecules as sirtuin inhibitors with anticancer activities**
BINARCI B., Kilic E. K., DOĞAN T., ATALAY R., KAHRAMAN D. C., BAYTAŞ S.
DRUG DEVELOPMENT RESEARCH, no.7, 2024 (SCI-Expanded)
II. **Mutual annotation-based prediction of protein domain functions with Domain2GO**

Ulusoy E., DOĞAN T.
PROTEIN SCIENCE, no.6, 2024 (SCI-Expanded)

III. **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, vol.169, 2024 (SCI-Expanded)

IV. **How to approach machine learning-based prediction of drug/compound–target interactions**
Atas Guvenilir H., DOĞAN T.
Journal of Cheminformatics, vol.15, no.1, 2023 (SCI-Expanded)

V. **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, vol.41, no.8, pp.1056-1059, 2023 (SCI-Expanded)

VI. **SELFormer: molecular representation learning via SELFIES language models**
Yüksel A., Ulusoy E., Ünlü A., DOĞAN T.
Machine Learning: Science and Technology, vol.4, no.2, 2023 (SCI-Expanded)

VII. **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, vol.24, no.2, 2023 (SCI-Expanded)

VIII. **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, vol.51, no.D1, 2023 (SCI-Expanded)

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

X. **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, vol.38, no.17, pp.4226-4229, 2022 (SCI-Expanded)

XI. **Learning functional properties of proteins with language models**
Unsal S., Atas H., Albayrak M., Turhan K., Acar A. C., Doğan T.
NATURE MACHINE INTELLIGENCE, vol.4, no.3, pp.227-245, 2022 (SCI-Expanded)

XII. **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, vol.17, no.12, pp.1425-1441, 2022 (SCI-Expanded)

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

XIV. **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, vol.19, no.12, 2021 (SCI-Expanded)

XV. **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, vol.17, no.11, 2021 (SCI-Expanded)

XVI. **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, vol.49, no.16, 2021 (SCI-Expanded)

XVII. **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, vol.12, no.1, 2021 (SCI-Expanded)

XVIII. **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, vol.37, no.5, pp.693-704, 2021 (SCI-Expanded)

XIX. **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, vol.49, no.D1, 2021 (SCI-Expanded)

XX. **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, vol.36, no.14, pp.4227-4230, 2020 (SCI-Expanded)

XXI. **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, vol.11, no.9, pp.2531-2557, 2020 (SCI-Expanded)

XXII. **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, vol.20, no.1, 2019 (SCI-Expanded)

XXIII. **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, vol.6, 2019 (SCI-Expanded)

XXIV. **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, vol.20, no.5, pp.1878-1912, 2019 (SCI-Expanded)

XXV. **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, vol.9, 2019 (SCI-Expanded)

XXVI. **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, vol.47, 2019 (SCI-Expanded)

XXVII. **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, vol.19, 2018 (SCI-Expanded)

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

XXIX. **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, vol.86, no.2, pp.135-151, 2018 (SCI-Expanded)

XXX. **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, vol.18, no.8, pp.700-713, 2018 (SCI-Expanded)

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

XXXII. **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, vol.33, no.21, pp.3454-3460, 2017 (SCI-Expanded)

XXXIII. **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, vol.474, pp.493-515, 2017 (SCI-Expanded)

XXXIV. **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, vol.45, 2017 (SCI-Expanded)

XXXV. **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, vol.17, 2016 (SCI-Expanded)

XXXVI. **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, vol.32, no.15, pp.2264-2271, 2016 (SCI-Expanded)

XXXVII. **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)

XXXVIII. **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, vol.44, 2016 (SCI-Expanded)

XXXIX. **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, vol.43, 2015 (SCI-Expanded)

XL. **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, vol.42, 2014 (SCI-Expanded)

XLI. **Automatic Identification of Highly Conserved Family Regions and Relationships in Genome Wide Datasets Including Remote Protein Sequences**
Doğan T., Karacali B.
PLOS ONE, vol.8, no.9, 2013 (SCI-Expanded)

Articles Published in Other Journals

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), vol.39, no.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, vol.52, no.4, pp.1266-1276, 2021 (Peer-Reviewed Journal)

Refereed Congress / Symposium Publications in Proceedings

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 June 2020, vol.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, United States Of America, 9 - 12 September 2015, pp.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, Austria, 13 - 15 February 2013, pp.1-8

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

Supported Projects

Doğan T., TUBITAK Project, Integrative Representation and Deep Graph Learning Based Prediction of Complex and Heterogeneous Relationships in Biomolecular and Biomedical Data, 2021 - 2024
Doğan T., TUBITAK Project, Çekişmeli Çizge Üretici Derin Sinir Ağları ile Hastalık Hedefli Yeni İlaç Adayı Moleküllerin De Novo Tasarımı, 2021 - 2024
Doğan T., Newton Programme Project, Derin Öğrenme Teknikleri Ve Ağ Analizi Yöntemleriyle Hazırlanmış Kapsamlı Biyomedikal İlişkiler Kaynağı, 2017 - 2020
Doğan T., Other International Funding Programs, Development of computational pipelines for drug discovery and repurposing, 2014 - 2018
Doğan T., Other International Funding Programs, Novel computational approaches for functional annotation of large data sets of proteins, 2013 - 2015

Metrics

Publication: 48
Citation (WoS): 17299
Citation (Scopus): 22060
H-Index (WoS): 21
H-Index (Scopus): 21