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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

Associate Professor, Hacettepe University, Bilişim Enstitüsü, Sağlık Bilişimi A.B.D., 2019 - Continues

Articles Published in Journals That Entered SCI, SSCI and AHCI Indexes

- I. **DEEPScreen: high performance drug-target interaction prediction with convolutional neural networks using 2-D structural compound representations**
RİFAİOĞLU A. S. , NALBAT E., Atalay V., Martin M. J. , Cetin-Atalay R., DOĞAN T.
CHEMICAL SCIENCE, vol.11, pp.2531-2557, 2020 (Journal Indexed in SCI)
- II. **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. , Kacsóh B. Z. , Crocker A. W. , Lewis K. A. , Georghiou G., Nguyen H. N. , Hamid M. N. , et al.
GENOME BIOLOGY, vol.20, 2019 (Journal Indexed in SCI)
- III. **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 (Journal Indexed in SCI)
- IV. **Recent applications of deep learning and machine intelligence on in silico drug discovery: methods, tools and databases**
RİFAİOĞLU A. S. , Atas H., Martin M. J. , Cetin-Atalay R., Atalay V., Dogan T.
BRIEFINGS IN BIOINFORMATICS, vol.20, pp.1878-1912, 2019 (Journal Indexed in SCI)
- V. **DEEPred: Automated Protein Function Prediction with Multi-task Feed-forward Deep Neural Networks**
RİFAİOĞLU A. S. , Dogan T., Martin M. J. , Cetin-Atalay R., Atalay V.
SCIENTIFIC REPORTS, vol.9, 2019 (Journal Indexed in SCI)
- VI. **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 (Journal Indexed in SCI)
- VII. **ECPred: a tool for the prediction of the enzymatic functions of protein sequences based on the EC nomenclature**
DALKIRAN A., RİFAİOĞLU A. S. , Martin M. J. , Cetin-Atalay R., Atalay V., Dogan T.
BMC BIOINFORMATICS, vol.19, 2018 (Journal Indexed in SCI)

- VIII. **HPO2GO: prediction of human phenotype ontology term associations for proteins using cross ontology annotation co-occurrences**
Dogana T.
PEERJ, vol.6, 2018 (Journal Indexed in SCI)
- IX. **Large-scale automated function prediction of protein sequences and an experimental case study validation on PTEN transcript variants**
RİFAİOĞLU A. S. , Dogana T., Sarac O. S. , Ersahin T., Saidi R., ATALAY M. V. , Martin M. J. , Cetin-Atalay R.
PROTEINS-STRUCTURE FUNCTION AND BIOINFORMATICS, vol.86, pp.135-151, 2018 (Journal Indexed in SCI)
- X. **A Structural Perspective on the Modulation of Protein-protein Interactions with Small Molecules**
Demirel H. C. , Dogana T., TUNÇBAĞ N.
CURRENT TOPICS IN MEDICINAL CHEMISTRY, vol.18, pp.700-713, 2018 (Journal Indexed in SCI)
- XI. **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, pp.3454-3460, 2017 (Journal Indexed in SCI)
- XII. **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 (Journal Indexed in SCI)
- XIII. **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 (Journal Indexed in SCI)
- XIV. **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 (Journal Indexed in SCI)
- XV. **UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB**
Dogana T., MacDougall A., Saidi R., Poggioli D., Bateman A., O'Donovan C., Martin M. J.
BIOINFORMATICS, vol.32, pp.2264-2271, 2016 (Journal Indexed in SCI)
- XVI. **The UniProtKB guide to the human proteome**
Breuzza 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 (Journal Indexed in SCI)
- XVII. **Tools and data services registry: a community effort to document bioinformatics resources**
Ison J., Rapacki K., Menager H., Kalas M., Rydzka E., Chmura P., Anthon C., Beard N., Berka K., Bolser D., et al.
NUCLEIC ACIDS RESEARCH, vol.44, 2016 (Journal Indexed in SCI)
- XVIII. **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 (Journal Indexed in SCI)
- XIX. **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 (Journal Indexed in SCI)
- XX. **Automatic Identification of Highly Conserved Family Regions and Relationships in Genome Wide Datasets Including Remote Protein Sequences**
Dogana T., Karacali B.
PLOS ONE, vol.8, 2013 (Journal Indexed in SCI)

Refereed Congress / Symposium Publications in Proceedings

- I. **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
- II. **2-D thresholding of the connectivity map following the multiple sequence alignments of diverse datasets**
Doğan T., Karaçalı B.
10th IASTED International Conference on Biomedical Engineering, BioMed 2013, Innsbruck, Austria, 13 - 15 February 2013, pp.1-8
- III. **Evolutionary relationships between gene sequences via nonlinear embedding Doğrusal olmayan gömme teknikleri altında gen dizilerinin evrimsel ilişkileri**
Doğan T., Karaçalı B.
2010 15th National Biomedical Engineering Meeting, BIYOMUT2010, Antalya, Turkey, 21 - 24 April 2010

Citations

Total Citations (WOS):6395

h-index (WOS):10