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Kişisel Bilgiler

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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

Doç.Dr., Hacettepe Üniversitesi, Bilişim Enstitüsü, Sağlık Bilişimi A.B.D., 2019 - Devam Ediyor

SCI, SSCI ve AHCI İndekslerine Giren Dergilerde Yayınlanan Makaleler

- I. **MDeePred: novel multi-channel protein featurization for deep learning-based binding affinity prediction in drug discovery**
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- II. **iBioProVis: interactive visualization and analysis of compound bioactivity space**
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- III. **DEEPScreen: high performance drug-target interaction prediction with convolutional neural networks using 2-D structural compound representations**
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- IV. **The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens**
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- V. **FAIR adoption, assessment and challenges at UniProt**
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- VI. **Recent applications of deep learning and machine intelligence on in silico drug discovery: methods, tools and databases**
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- VII. **DEEPred: Automated Protein Function Prediction with Multi-task Feed-forward Deep Neural Networks**
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- VIII. **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.
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- IX. **ECPred: a tool for the prediction of the enzymatic functions of protein sequences based on the EC nomenclature**
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- X. **HPO2GO: prediction of human phenotype ontology term associations for proteins using cross ontology annotation co-occurrences**
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- XI. **Large-scale automated function prediction of protein sequences and an experimental case study validation on PTEN transcript variants**
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- XII. **A Structural Perspective on the Modulation of Protein-protein Interactions with Small Molecules**
Demirel H. C. , Dogan T., TUNÇBAĞ N.
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- XIII. **On expert curation and scalability: UniProtKB/Swiss-Prot as a case study**
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- XIV. **From the research laboratory to the database: the Caenorhabditis elegans kinome in UniProtKB**
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- XV. **UniProt: the universal protein knowledgebase**
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- XVI. **An expanded evaluation of protein function prediction methods shows an improvement in accuracy**
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- XVII. **UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB**
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- XVIII. **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.
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- XIX. **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.
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- XX. **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.
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- XXI. **Activities at the Universal Protein Resource (UniProt)**
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XXII. **Automatic Identification of Highly Conserved Family Regions and Relationships in Genome Wide Datasets Including Remote Protein Sequences**

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Hakemli Kongre / Sempozyum Bildiri Kitaplarında Yer Alan Yayınlar

I. **Unsupervised identification of redundant domain entries in InterPro database using clustering techniques**

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II. **2-D thresholding of the connectivity map following the multiple sequence alignments of diverse datasets**

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III. **Evolutionary relationships between gene sequences via nonlinear embedding Doğrusal olmayan gömme teknikleri altında gen dizilerinin evrimsel ilişkileri**

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Atıflar

Toplam Atıf Sayısı (WOS):6396

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