Tunca Dogan

List of Publications by Year in descending order

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34 papers	22,397 citations	430754 18 h-index	454834 30 g-index
44 all docs	44 docs citations	44 times ranked	40846 citing authors

#	Article	IF	Citations
1	Learning functional properties of proteins with language models. Nature Machine Intelligence, 2022, 4, 227-245.	8.3	72
2	SLPred: a multi-view subcellular localization prediction tool for multi-location human proteins. Bioinformatics, 2022, 38, 4226-4229.	1.8	3
3	MDeePred: novel multi-channel protein featurization for deep learning-based binding affinity prediction in drug discovery. Bioinformatics, 2021, 37, 693-704.	1.8	61
4	UniProt: the universal protein knowledgebase in 2021. Nucleic Acids Research, 2021, 49, D480-D489.	6.5	4,709
5	Crowdsourced mapping of unexplored target space of kinase inhibitors. Nature Communications, 2021, 12, 3307.	5.8	41
6	CROssBAR: comprehensive resource of biomedical relations with knowledge graph representations. Nucleic Acids Research, 2021, 49, e96-e96.	6.5	19
7	Protein domain-based prediction of drug/compoundâ€“target interactions and experimental validation on LIM kinases. PLoS Computational Biology, 2021, 17, e1009171.	1.5	13
8	Editorial: Machine Learning Methodologies to Study Molecular Interactions. Frontiers in Molecular Biosciences, 2021, 8, 806474.	1.6	1
9	A crowdsourcing open platform for literature curation in UniProt. PLoS Biology, 2021, 19, e3001464.	2.6	74
10	Data Centric Molecular Analysis and Evaluation of Hepatocellular Carcinoma Therapeutics Using Machine Intelligence-Based Tools. Journal of Gastrointestinal Cancer, 2021, 52, 1266-1276.	0.6	0
11	DEEPScreen: high performance drugâ€“target interaction prediction with convolutional neural networks using 2-D structural compound representations. Chemical Science, 2020, 11, 2531-2557.	3.7	131
12	iBioProVis: interactive visualization and analysis of compound bioactivity space. Bioinformatics, 2020, 36, 4227-4230.	1.8	7
13	Abstract 5235:In vitrovalidation of drug-target interactions revealedin silicoby Comprehensive Resource of Biomedical Relations with Network Representations and Deep Learning (CROssBAR) in HCC. , 2020, , .		0
14	Recent applications of deep learning and machine intelligence on in silico drug discovery: methods, tools and databases. Briefings in Bioinformatics, 2019, 20, 1878-1912.	3.2	310
15	FAIR adoption, assessment and challenges at UniProt. Scientific Data, 2019, 6, 175.	2.4	11
16	DEEPred: Automated Protein Function Prediction with Multi-task Feed-forward Deep Neural Networks. Scientific Reports, 2019, 9, 7344.	1.6	80
17	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	3.8	261
18	UniProt: a worldwide hub of protein knowledge. Nucleic Acids Research, 2019, 47, D506-D515.	6.5	6,185

#	Article	IF	Citations
19	Phylogenetic and Other Conservation-Based Approaches to Predict Protein Functional Sites. Methods in Molecular Biology, 2018, 1762, 51-69.	0.4	4
20	Largeâ€scale automated function prediction of protein sequences and an experimental case study validation on PTEN transcript variants. Proteins: Structure, Function and Bioinformatics, 2018, 86, 135-151.	1.5	13
21	HPO2GO: prediction of human phenotype ontology term associations for proteins using cross ontology annotation co-occurrences. PeerJ, 2018, 6, e5298.	0.9	27
22	ECPred: a tool for the prediction of the enzymatic functions of protein sequences based on the EC nomenclature. BMC Bioinformatics, 2018, 19, 334.	1.2	99
23	A Structural Perspective on the Modulation of Protein-Protein Interactions with Small Molecules. Current Topics in Medicinal Chemistry, 2018, 18, 700-713.	1.0	6
24	UniProt: the universal protein knowledgebase. Nucleic Acids Research, 2017, 45, D158-D169.	6.5	4,240
25	From the research laboratory to the database: the Caenorhabditis elegans kinome in UniProtKB. Biochemical Journal, 2017, 474, 493-515.	1.7	9
26	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
27	UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB. Bioinformatics, 2016, 32, 2264-2271.	1.8	37
28	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	6.5	113
29	Unsupervised identification of redundant domain entries in InterPro database using clustering techniques. , 2015, , .		0
30	UniProt: a hub for protein information. Nucleic Acids Research, 2015, 43, D204-D212.	6.5	4,370
31	Activities at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2014, 42, D191-D198.	6.5	1,162
32	Automatic Identification of Highly Conserved Family Regions and Relationships in Genome Wide Datasets Including Remote Protein Sequences. PLoS ONE, 2013, 8, e75458.	1.1	7
33	2-D Thresholding of the Connectivity Map Following the Multiple Sequence Alignments of Diverse Datasets. , 2013, , .		0
34	Evolutionary relationships between gene sequences via nonlinear embedding. , 2010, , .		0