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	UniProt: a worldwide hub of protein knowledge. Nucleic Acids Research, 2019, 47, D506-D515.	6.5	6,185
2	UniProt: the universal protein knowledgebase in 2021. Nucleic Acids Research, 2021, 49, D480-D489.	6.5	4,709
3	UniProt: a hub for protein information. Nucleic Acids Research, 2015, 43, D204-D212.	6.5	4,370
4	UniProt: the universal protein knowledgebase. Nucleic Acids Research, 2017, 45, D158-D169.	6.5	4,240
5	Activities at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2014, 42, D191-D198.	6.5	1,162
6	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
7	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
8	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
9	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
10	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	6.5	113
11	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
12	DEEPred: Automated Protein Function Prediction with Multi-task Feed-forward Deep Neural Networks. Scientific Reports, 2019, 9, 7344.	1.6	80
13	A crowdsourcing open platform for literature curation in UniProt. PLoS Biology, 2021, 19, e3001464.	2.6	74
14	Learning functional properties of proteins with language models. Nature Machine Intelligence, 2022, 4, 227-245.	8.3	72
15	MDeePred: novel multi-channel protein featurization for deep learning-based binding affinity prediction in drug discovery. Bioinformatics, 2021, 37, 693-704.	1.8	61
16	Crowdsourced mapping of unexplored target space of kinase inhibitors. Nature Communications, 2021, 12, 3307.	5.8	41
17	UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB. Bioinformatics, 2016, 32, 2264-2271.	1.8	37
18	HPO2GO: prediction of human phenotype ontology term associations for proteins using cross ontology annotation co-occurrences. PeerJ, 2018, 6, e5298.	0.9	27

#	Article	IF	Citations
19	CROssBAR: comprehensive resource of biomedical relations with knowledge graph representations. Nucleic Acids Research, 2021, 49, e96-e96.	6.5	19
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	Protein domain-based prediction of drug/compoundâ€“target interactions and experimental validation on LIM kinases. PLoS Computational Biology, 2021, 17, e1009171.	1.5	13
22	FAIR adoption, assessment and challenges at UniProt. Scientific Data, 2019, 6, 175.	2.4	11
23	From the research laboratory to the database: the Caenorhabditis elegans kinome in UniProtKB. Biochemical Journal, 2017, 474, 493-515.	1.7	9
24	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
25	iBioProVis: interactive visualization and analysis of compound bioactivity space. Bioinformatics, 2020, 36, 4227-4230.	1.8	7
26	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
27	Phylogenetic and Other Conservation-Based Approaches to Predict Protein Functional Sites. Methods in Molecular Biology, 2018, 1762, 51-69.	0.4	4
28	SLPred: a multi-view subcellular localization prediction tool for multi-location human proteins. Bioinformatics, 2022, 38, 4226-4229.	1.8	3
29	Editorial: Machine Learning Methodologies to Study Molecular Interactions. Frontiers in Molecular Biosciences, 2021, 8, 806474.	1.6	1
30	Evolutionary relationships between gene sequences via nonlinear embedding. , 2010, , .		0
31	Unsupervised identification of redundant domain entries in InterPro database using clustering techniques. , 2015, , .		0
32	2-D Thresholding of the Connectivity Map Following the Multiple Sequence Alignments of Diverse Datasets. , 2013, , .		0
33	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
34	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