

Christian Dallago

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9407717/publications.pdf>

Version: 2024-02-01

21
papers

2,097
citations

687363

13
h-index

752698

20
g-index

36
all docs

36
docs citations

36
times ranked

1621
citing authors

#	ARTICLE	IF	CITATIONS
1	ProtTrans: Toward Understanding the Language of Life Through Self-Supervised Learning. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2022, 44, 7112-7127.	13.9	496
2	ProteomicsDB: toward a FAIR open-source resource for life-science research. Nucleic Acids Research, 2022, 50, D1541-D1552.	14.5	35
3	Embeddings from protein language models predict conservation and variant effects. Human Genetics, 2022, 141, 1629-1647.	3.8	60
4	PredictProtein - Predicting Protein Structure and Function for 29 Years. Nucleic Acids Research, 2021, 49, W535-W540.	14.5	135
5	Clustering FunFams using sequence embeddings improves EC purity. Bioinformatics, 2021, 37, 3449-3455.	4.1	25
6	Learned Embeddings from Deep Learning to Visualize and Predict Protein Sets. Current Protocols, 2021, 1, e113.	2.9	61
7	SARS-CoV-2 structural coverage map reveals viral protein assembly, mimicry, and hijacking mechanisms. Molecular Systems Biology, 2021, 17, e10079.	7.2	22
8	Embeddings from deep learning transfer GO annotations beyond homology. Scientific Reports, 2021, 11, 1160.	3.3	95
9	Protein matchmaking through representation learning. Cell Systems, 2021, 12, 948-950.	6.2	0
10	Light attention predicts protein location from the language of life. Bioinformatics Advances, 2021, 1, .	2.4	57
11	A flexible search system for high-accuracy identification of biological entities and molecules. Journal of Open Source Software, 2021, 6, 3756.	4.6	1
12	Author-sourced capture of pathway knowledge in computable form using Biofactoid. ELife, 2021, 10, .	6.0	11
13	Protein embeddings and deep learning predict binding residues for various ligand classes. Scientific Reports, 2021, 11, 23916.	3.3	63
14	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. Nucleic Acids Research, 2020, 48, D489-D497.	14.5	161
15	Visualizing Human Protein-Protein Interactions and Subcellular Localizations on Cell Images Through CellMap. Current Protocols in Bioinformatics, 2020, 69, e97.	25.8	6
16	AlignmentViewer: Sequence Analysis of Large Protein Families. F1000Research, 2020, 9, 213.	1.6	5
17	AlignmentViewer: Sequence Analysis of Large Protein Families. F1000Research, 2020, 9, 213.	1.6	7
18	Modeling aspects of the language of life through transfer-learning protein sequences. BMC Bioinformatics, 2019, 20, 723.	2.6	319

#	ARTICLE	IF	CITATIONS
19	The EVcouplings Python framework for coevolutionary sequence analysis. <i>Bioinformatics</i> , 2019, 35, 1582-1584.	4.1	180
20	CellMap visualizes protein-protein interactions and subcellular localization. <i>F1000Research</i> , 2017, 6, 1824.	1.6	6
21	CellMap visualizes protein-protein interactions and subcellular localization. <i>F1000Research</i> , 2017, 6, 1824.	1.6	5