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List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5236582/publications.pdf

Version: 2024-02-01

21	465	933447 10	794594 19
papers	citations	h-index	g-index

23	23	23	528
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	PyUUL provides an interface between biological structures and deep learning algorithms. Nature Communications, 2022, 13, 961.	12.8	10
2	Prediction of Disordered Regions in Proteins with Recurrent Neural Networks and Protein Dynamics. Journal of Molecular Biology, 2022, 434, 167579.	4.2	22
3	HPMPdb: a machine learning-ready database of protein molecular phenotypes associated to human missense variants. Current Research in Structural Biology, 2022, , .	2.2	1
4	Role and therapeutic potential of liquidâ€“liquid phase separation in amyotrophic lateral sclerosis. Journal of Molecular Cell Biology, 2021, 13, 15-28.	3.3	23
5	b2bTools: online predictions for protein biophysical features and their conservation. Nucleic Acids Research, 2021, 49, W52-W59.	14.5	9
6	In silico prediction of in vitro protein liquidâ€“liquid phase separation experiments outcomes with multi-head neural attention. Bioinformatics, 2021, 37, 3473-3479.	4.1	14
7	Accurate prediction of protein beta-aggregation with generalized statistical potentials. Bioinformatics, 2020, 36, 2076-2081.	4.1	20
8	ShiftCrypt: a web server to understand and biophysically align proteins through their NMR chemical shift values. Nucleic Acids Research, 2020, 48, W36-W40.	14.5	1
9	Structure-based machine-guided mapping of amyloid sequence space reveals uncharted sequence clusters with higher solubilities. Nature Communications, 2020, 11, 3314.	12.8	54
10	Insight into the protein solubility driving forces with neural attention. PLoS Computational Biology, 2020, 16, e1007722.	3.2	25
11	Auto-encoding NMR chemical shifts from their native vector space to a residue-level biophysical index. Nature Communications, 2019, 10, 2511.	12.8	5
12	Computational identification of prion-like RNA-binding proteins that form liquid phase-separated condensates. Bioinformatics, 2019, 35, 4617-4623.	4.1	45
13	Exploring the limitations of biophysical propensity scales coupled with machine learning for protein sequence analysis. Scientific Reports, 2019, 9, 16932.	3.3	19
14	Large-scale in-silico statistical mutagenesis analysis sheds light on the deleteriousness landscape of the human proteome. Scientific Reports, 2018, 8, 16980.	3.3	7
15	Ultra-fast global homology detection with Discrete Cosine Transform and Dynamic Time Warping. Bioinformatics, 2018, 34, 3118-3125.	4.1	13
16	Exploring the Sequence-based Prediction of Folding Initiation Sites in Proteins. Scientific Reports, 2017, 7, 8826.	3.3	39
17	SVM-dependent pairwise HMM: an application to protein pairwise alignments. Bioinformatics, 2017, 33, 3902-3908.	4.1	8
18	DEOGEN2: prediction and interactive visualization of single amino acid variant deleteriousness in human proteins. Nucleic Acids Research, 2017, 45, W201-W206.	14.5	114

#	Article	IF	Citations
19	Investigating the Molecular Mechanisms Behind Uncharacterized Cysteine Losses from Prediction of Their Oxidation State. Human Mutation, 2017, 38, 86-94.	2.5	4
20	Clustering-based model of cysteine co-evolution improves disulfide bond connectivity prediction and reduces homologous sequence requirements. Bioinformatics, 2015, 31, 1219-1225.	4.1	10
21	An Evolutionary View on Disulfide Bond Connectivities Prediction Using Phylogenetic Trees and a Simple Cysteine Mutation Model. PLoS ONE, 2015, 10, e0131792.	2.5	11