

Konstantinos D Tsirigos

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

6,577
citations

567281

15
h-index

713466

21
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all docs

23
docs citations

23
times ranked

9532
citing authors

#	ARTICLE	IF	CITATIONS
1	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019, 37, 420-423.	17.5	3,317
2	SignalP 6.0 predicts all five types of signal peptides using protein language models. <i>Nature Biotechnology</i> , 2022, 40, 1023-1025.	17.5	883
3	The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides. <i>Nucleic Acids Research</i> , 2015, 43, W401-W407.	14.5	776
4	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	14.5	242
5	Combined prediction of Tat and Sec signal peptides with hidden Markov models. <i>Bioinformatics</i> , 2010, 26, 2811-2817.	4.1	217
6	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019, 38, 200-216.	1.6	154
7	Prediction of Lipoprotein Signal Peptides in Gram-Positive Bacteria with a Hidden Markov Model. <i>Journal of Proteome Research</i> , 2008, 7, 5082-5093.	3.7	135
8	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	14.5	117
9	PRED-TMBB2: improved topology prediction and detection of beta-barrel outer membrane proteins. <i>Bioinformatics</i> , 2016, 32, i665-i671.	4.1	77
10	Inclusion of dyad-repeat pattern improves topology prediction of transmembrane β -barrel proteins. <i>Bioinformatics</i> , 2016, 32, 1571-1573.	4.1	75
11	Improved topology prediction using the terminal hydrophobic helices rule. <i>Bioinformatics</i> , 2016, 32, 1158-1162.	4.1	40
12	Topology of membrane proteins " predictions, limitations and variations. <i>Current Opinion in Structural Biology</i> , 2018, 50, 9-17.	5.7	31
13	A guideline to proteome-wide β -helical membrane protein topology predictions. <i>Proteomics</i> , 2012, 12, 2282-2294.	2.2	29
14	PREDICTION OF CELL WALL SORTING SIGNALS IN GRAM-POSITIVE BACTERIA WITH A HIDDEN MARKOV MODEL: APPLICATION TO COMPLETE GENOMES. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 387-401.	0.8	28
15	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav063.	3.0	8
16	GWAR: robust analysis and meta-analysis of genome-wide association studies. <i>Bioinformatics</i> , 2017, 33, 1521-1527.	4.1	8
17	Extending hidden Markov models to allow conditioning on previous observations. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1850019.	0.8	8
18	Large Tilts in Transmembrane Helices Can Be Induced during Tertiary Structure Formation. <i>Journal of Molecular Biology</i> , 2014, 426, 2529-2538.	4.2	5

#	ARTICLE	IF	CITATIONS
19	Hidden neural networks for transmembrane protein topology prediction. Computational and Structural Biotechnology Journal, 2021, 19, 6090-6097.	4.1	5
20	JUCHMME: a Java Utility for Class Hidden Markov Models and Extensions for biological sequence analysis. Bioinformatics, 2019, 35, 5309-5312.	4.1	4