

Konstantinos D Tsirigos

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

21
papers

2,873
citations

15
h-index

23
g-index

23
ext. papers

4,948
ext. citations

11.3
avg, IF

5.54
L-index

#	Paper	IF	Citations
21	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019 , 37, 420-423	44.5	1536
20	The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides. <i>Nucleic Acids Research</i> , 2015 , 43, W401-7	20.1	492
19	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017 , 45, D219-D227	20.1	182
18	Combined prediction of Tat and Sec signal peptides with hidden Markov models. <i>Bioinformatics</i> , 2010 , 26, 2811-7	7.2	165
17	Prediction of lipoprotein signal peptides in Gram-positive bacteria with a Hidden Markov Model. <i>Journal of Proteome Research</i> , 2008 , 7, 5082-93	5.6	101
16	SignalP 6.0 predicts all five types of signal peptides using protein language models.. <i>Nature Biotechnology</i> , 2022 ,	44.5	56
15	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019 , 38, 200-216	3.9	55
14	Inclusion of dyad-repeat pattern improves topology prediction of transmembrane β barrel proteins. <i>Bioinformatics</i> , 2016 , 32, 1571-3	7.2	47
13	PRED-TMBB2: improved topology prediction and detection of beta-barrel outer membrane proteins. <i>Bioinformatics</i> , 2016 , 32, i665-i671	7.2	47
12	Improved topology prediction using the terminal hydrophobic helices rule. <i>Bioinformatics</i> , 2016 , 32, 1158-62	7.2	26
11	A guideline to proteome-wide β helical membrane protein topology predictions. <i>Proteomics</i> , 2012 , 12, 2282-94	4.8	26
10	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 , 6, 387-401 ¹		21
9	Topology of membrane proteins-predictions, limitations and variations. <i>Current Opinion in Structural Biology</i> , 2018 , 50, 9-17	8.1	20
8	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2021 ,	20.1	13
7	Extending hidden Markov models to allow conditioning on previous observations. <i>Journal of Bioinformatics and Computational Biology</i> , 2018 , 16, 1850019	1	5
6	Large tilts in transmembrane helices can be induced during tertiary structure formation. <i>Journal of Molecular Biology</i> , 2014 , 426, 2529-38	6.5	5
5	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav063	5	5

4	GWAR: robust analysis and meta-analysis of genome-wide association studies. <i>Bioinformatics</i> , 2017 , 33, 1521-1527	7.2	3
3	JUCHMME: a Java Utility for Class Hidden Markov Models and Extensions for biological sequence analysis. <i>Bioinformatics</i> , 2019 , 35, 5309-5312	7.2	2
2	Hidden neural networks for transmembrane protein topology prediction. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 6090-6097	6.8	2
1	SignalP 6.0 achieves signal peptide prediction across all types using protein language models		2