

# Konstantinos D Tsirigos

## List of Publications by Year in Descending Order

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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 6.0 predicts all five types of signal peptides using protein language models.. <i>Nature Biotechnology</i> , <b>2022</b> ,	44.5	56
20	Hidden neural networks for transmembrane protein topology prediction. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 6090-6097	6.8	2
19	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , <b>2021</b> ,	20.1	13
18	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , <b>2019</b> , 38, 200-216	3.9	55
17	JUCHMME: a Java Utility for Class Hidden Markov Models and Extensions for biological sequence analysis. <i>Bioinformatics</i> , <b>2019</b> , 35, 5309-5312	7.2	2
16	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 420-423	44.5	1536
15	Extending hidden Markov models to allow conditioning on previous observations. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2018</b> , 16, 1850019	1	5
14	Topology of membrane proteins-predictions, limitations and variations. <i>Current Opinion in Structural Biology</i> , <b>2018</b> , 50, 9-17	8.1	20
13	GWAR: robust analysis and meta-analysis of genome-wide association studies. <i>Bioinformatics</i> , <b>2017</b> , 33, 1521-1527	7.2	3
12	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D219-D227	20.1	182
11	Inclusion of dyad-repeat pattern improves topology prediction of transmembrane $\beta$ barrel proteins. <i>Bioinformatics</i> , <b>2016</b> , 32, 1571-3	7.2	47
10	Improved topology prediction using the terminal hydrophobic helices rule. <i>Bioinformatics</i> , <b>2016</b> , 32, 1158-62	7.2	26
9	PRED-TMBB2: improved topology prediction and detection of beta-barrel outer membrane proteins. <i>Bioinformatics</i> , <b>2016</b> , 32, i665-i671	7.2	47
8	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> , <b>2015</b> , 2015, bav063	5	5
7	The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W401-7	20.1	492
6	Large tilts in transmembrane helices can be induced during tertiary structure formation. <i>Journal of Molecular Biology</i> , <b>2014</b> , 426, 2529-38	6.5	5
5	A guideline to proteome-wide $\beta$ helical membrane protein topology predictions. <i>Proteomics</i> , <b>2012</b> , 12, 2282-94	4.8	26

4	Combined prediction of Tat and Sec signal peptides with hidden Markov models. <i>Bioinformatics</i> , <b>2010</b> , 26, 2811-7	7.2	165
3	Prediction of lipoprotein signal peptides in Gram-positive bacteria with a Hidden Markov Model. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 5082-93	5.6	101
2	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> , <b>2008</b> , 6, 387-401 <sup>1</sup>		21
1	SignalP 6.0 achieves signal peptide prediction across all types using protein language models		2