

Henrik Nielsen

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.

35 papers	25,993 citations	21 h-index	40 g-index
40 ext. papers	31,334 ext. citations	9.5 avg, IF	7.34 L-index

#	Paper	IF	Citations
35	SignalP 6.0 predicts all five types of signal peptides using protein language models.. <i>Nature Biotechnology</i> , 2022 ,	44.5	56
34	DeepLoc 2.0: multi-label subcellular localization prediction using protein language models.. <i>Nucleic Acids Research</i> , 2022 ,	20.1	10
33	Deep protein representations enable recombinant protein expression prediction. <i>Computational Biology and Chemistry</i> , 2021 , 95, 107596	3.6	2
32	iMLP, a predictor for internal matrix targeting-like sequences in mitochondrial proteins. <i>Biological Chemistry</i> , 2021 , 402, 937-943	4.5	2
31	Spectrum of Protein Location in Proteomes Captures Evolutionary Relationship Between Species. <i>Journal of Molecular Evolution</i> , 2021 , 89, 544-553	3.1	1
30	Prediction of GPI-anchored proteins with pointer neural networks. <i>Current Research in Biotechnology</i> , 2021 , 3, 6-13	4.8	14
29	Landscape of Eukaryotic Transmembrane Beta Barrel Proteins. <i>Journal of Proteome Research</i> , 2020 , 19, 1209-1221	5.6	2
28	Predicting eukaryotic protein secretion without signals. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019 , 1867, 140174	4	10
27	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019 , 38, 200-216	3.9	55
26	Detecting sequence signals in targeting peptides using deep learning. <i>Life Science Alliance</i> , 2019 , 2,	5.8	183
25	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019 , 37, 420-423	44.5	1536
24	NetSurfP-2.0: Improved prediction of protein structural features by integrated deep learning. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 520-527	4.2	214
23	Comparative genomics of <i>Campylobacter concisus</i> : Analysis of clinical strains reveals genome diversity and pathogenic potential. <i>Emerging Microbes and Infections</i> , 2018 , 7, 116	18.9	16
22	Predicting Secretory Proteins with SignalP. <i>Methods in Molecular Biology</i> , 2017 , 1611, 59-73	1.4	475
21	An introduction to deep learning on biological sequence data: examples and solutions. <i>Bioinformatics</i> , 2017 , 33, 3685-3690	7.2	81
20	Protein Sorting Prediction. <i>Methods in Molecular Biology</i> , 2017 , 1615, 23-57	1.4	5
19	DeepLoc: prediction of protein subcellular localization using deep learning. <i>Bioinformatics</i> , 2017 , 33, 3387-3395	7.2	460

18	Predicting Subcellular Localization of Proteins by Bioinformatic Algorithms. <i>Current Topics in Microbiology and Immunology</i> , 2017 , 404, 129-158	3.3	7
17	Convolutional LSTM Networks for Subcellular Localization of Proteins. <i>Lecture Notes in Computer Science</i> , 2015 , 68-80	0.9	54
16	LocTree3 prediction of localization. <i>Nucleic Acids Research</i> , 2014 , 42, W350-5	20.1	183
15	SignalP 4.0: discriminating signal peptides from transmembrane regions. <i>Nature Methods</i> , 2011 , 8, 785-621.6	6.2	6866
14	Locating proteins in the cell using TargetP, SignalP and related tools. <i>Nature Protocols</i> , 2007 , 2, 953-71	18.8	2596
13	An overabundance of phase 0 introns immediately after the start codon in eukaryotic genes. <i>BMC Genomics</i> , 2006 , 7, 256	4.5	9
12	Prediction of twin-arginine signal peptides. <i>BMC Bioinformatics</i> , 2005 , 6, 167	3.6	408
11	Improved prediction of signal peptides: SignalP 3.0. <i>Journal of Molecular Biology</i> , 2004 , 340, 783-95	6.5	5563
10	Prediction of lipoprotein signal peptides in Gram-negative bacteria. <i>Protein Science</i> , 2003 , 12, 1652-62	6.3	880
9	Predicting subcellular localization of proteins based on their N-terminal amino acid sequence. <i>Journal of Molecular Biology</i> , 2000 , 300, 1005-16	6.5	3635
8	Machine learning approaches for the prediction of signal peptides and other protein sorting signals. <i>Protein Engineering, Design and Selection</i> , 1999 , 12, 3-9	1.9	461
7	ChloroP, a neural network-based method for predicting chloroplast transit peptides and their cleavage sites. <i>Protein Science</i> , 1999 , 8, 978-84	6.3	1551
6	A neural network method for identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. <i>International Journal of Neural Systems</i> , 1997 , 8, 581-99	6.2	552
5	Defining a similarity threshold for a functional protein sequence pattern: the signal peptide cleavage site. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 24, 165-77	4.2	61
4	Language modelling for biological sequences [t]urated datasets and baselines		2
3	NetSurfP-2.0: improved prediction of protein structural features by integrated deep learning		8
2	Prediction of GPI-Anchored proteins with pointer neural networks		1
1	SignalP 6.0 achieves signal peptide prediction across all types using protein language models		2

