

HÃ¥kan Viklund

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10663017/publications.pdf>

Version: 2024-02-01

10
papers

1,778
citations

1039880

9
h-index

1372474

10
g-index

10
all docs

10
docs citations

10
times ranked

2515
citing authors

#	ARTICLE	IF	CITATIONS
1	TOPCONS: consensus prediction of membrane protein topology. <i>Nucleic Acids Research</i> , 2009, 37, W465-W468.	6.5	487
2	Remote homology detection of integral membrane proteins using conserved sequence features. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1387-1399.	1.5	9
3	Estimating the length of transmembrane helices using Z-coordinate predictions. <i>Protein Science</i> , 2008, 17, 271-278.	3.1	27
4	Prediction of membrane-protein topology from first principles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7177-7181.	3.3	288
5	SPOCTOPUS: a combined predictor of signal peptides and membrane protein topology. <i>Bioinformatics</i> , 2008, 24, 2928-2929.	1.8	213
6	OCTOPUS: improving topology prediction by two-track ANN-based preference scores and an extended topological grammar. <i>Bioinformatics</i> , 2008, 24, 1662-1668.	1.8	349
7	Structural Classification and Prediction of Reentrant Regions in α -Helical Transmembrane Proteins: Application to Complete Genomes. <i>Journal of Molecular Biology</i> , 2006, 361, 591-603.	2.0	83
8	PONGO: a web server for multiple predictions of all-alpha transmembrane proteins. <i>Nucleic Acids Research</i> , 2006, 34, W169-W172.	6.5	37
9	ZPRED: Predicting the distance to the membrane center for residues in α -helical membrane proteins. <i>Bioinformatics</i> , 2006, 22, e191-e196.	1.8	50
10	Best α -helical transmembrane protein topology predictions are achieved using hidden Markov models and evolutionary information. <i>Protein Science</i> , 2004, 13, 1908-1917.	3.1	235