

# 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  | 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       |
| 3  | 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       |
| 4  | Best $\alpha$ -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       |
| 5  | SPECTOPUS: a combined predictor of signal peptides and membrane protein topology. <i>Bioinformatics</i> , 2008, 24, 2928-2929.  | 1.8 | 213       |
| 6  | Structural Classification and Prediction of Reentrant Regions in $\alpha$ -Helical Transmembrane Proteins: Application to Complete Genomes. <i>Journal of Molecular Biology</i> , 2006, 361, 591-603. | 2.0 | 83        |
| 7  | ZPRED: Predicting the distance to the membrane center for residues in $\alpha$ -helical membrane proteins. <i>Bioinformatics</i> , 2006, 22, e191-e196.   | 1.8 | 50        |
| 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  | Estimating the length of transmembrane helices using $\alpha$ -coordinate predictions. <i>Protein Science</i> , 2008, 17, 271-278.  | 3.1 | 27        |
| 10 | 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         |