

# Nils Woetzel

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11752893/publications.pdf>

Version: 2024-02-01

14  
papers

692  
citations

933447

10  
h-index

1281871

11  
g-index

14  
all docs

14  
docs citations

14  
times ranked

1086  
citing authors

#	ARTICLE	IF	CITATIONS
1	Solvent accessible surface area approximations for rapid and accurate protein structure prediction. <i>Journal of Molecular Modeling</i> , 2009, 15, 1093-1108.	1.8	222
2	Bcl::Cluster: A method for clustering biological molecules coupled with visualization in the Pymol Molecular Graphics System. , 2011, 2011, 13-18.		146
3	Simultaneous prediction of protein secondary structure and transmembrane spans. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1127-1140.	2.6	56
4	A unified hydrophobicity scale for multispan membrane proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 13-29.	2.6	51
5	BCL::Fold - De Novo Prediction of Complex and Large Protein Topologies by Assembly of Secondary Structure Elements. <i>PLoS ONE</i> , 2012, 7, e49240.	2.5	41
6	BCL::Scoreâ€”Knowledge Based Energy Potentials for Ranking Protein Models Represented by Idealized Secondary Structure Elements. <i>PLoS ONE</i> , 2012, 7, e49242.	2.5	40
7	BCL::MP-Fold: Folding Membrane Proteins through Assembly of Transmembrane Helices. <i>Structure</i> , 2013, 21, 1107-1117.	3.3	35
8	BCL::EM-Fit: Rigid body fitting of atomic structures into density maps using geometric hashing and real space refinement. <i>Journal of Structural Biology</i> , 2011, 175, 264-276.	2.8	33
9	BCL::MPâ€”fold: Membrane protein structure prediction guided by <sc>EPR</sc> restraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1947-1962.	2.6	24
10	BCL::Foldâ€”Protein topology determination from limited NMR restraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 587-595.	2.6	21
11	BCL::SAXS: GPU accelerated Debye method for computation of small angle X-ray scattering profiles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1500-1512.	2.6	13
12	Structure and mechanism of the phage T4 recombination mediator protein UvsY. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3275-3280.	7.1	10
13	Poster: GPU-accelerated rigid body fitting of atomic structures into electron density maps. , 2011, , .		0
14	Poster: GPU-accelerated artificial neural network for QSAR modeling. , 2011, , .		0