Nils Woetzel

List of Publications by Year
in descending order

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