

# Björn Wallner

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

2,955  
citations

257450

24  
h-index

395702

33  
g-index

37  
all docs

37  
docs citations

37  
times ranked

3481  
citing authors

#	ARTICLE	IF	CITATIONS
1	The MYC oncoprotein directly interacts with its chromatin cofactor PNUTS to recruit PP1 phosphatase. <i>Nucleic Acids Research</i> , 2022, 50, 3505-3522.	14.5	11
2	InterPepScore: a deep learning score for improving the FlexPepDock refinement protocol. <i>Bioinformatics</i> , 2022, 38, 3209-3215.	4.1	1
3	InterPep2: global peptide-protein docking using interaction surface templates. <i>Bioinformatics</i> , 2020, 36, 2458-2465.	4.1	30
4	InterLig: improved ligand-based virtual screening using topologically independent structural alignments. <i>Bioinformatics</i> , 2020, 36, 3266-3267.	4.1	4
5	Estimation of model accuracy in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1361-1377.	2.6	78
6	rawMSA: End-to-end Deep Learning using raw Multiple Sequence Alignments. <i>PLoS ONE</i> , 2019, 14, e0220182.	2.5	62
7	Predicting protein-peptide interaction sites using distant protein complexes as structural templates. <i>Scientific Reports</i> , 2019, 9, 4267.	3.3	44
8	Improved protein model quality assessments by changing the target function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 654-663.	2.6	11
9	Methods for estimation of model accuracy in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 361-373.	2.6	27
10	InterPred: A pipeline to identify and model protein-protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1159-1170.	2.6	32
11	Proteus: a random forest classifier to predict disorder-to-order transitioning binding regions in intrinsically disordered proteins. <i>Journal of Computer-Aided Molecular Design</i> , 2017, 31, 453-466.	2.9	31
12	DockQ: A Quality Measure for Protein-Protein Docking Models. <i>PLoS ONE</i> , 2016, 11, e0161879.	2.5	205
13	Charge Pair Interactions in Transmembrane Helices and Turn Propensity of the Connecting Sequence Promote Helical Hairpin Insertion. <i>Journal of Molecular Biology</i> , 2013, 425, 830-840.	4.2	30
14	Improved model quality assessment using ProQ2. <i>BMC Bioinformatics</i> , 2012, 13, 224.	2.6	173
15	The Free Energy Barrier for Arginine Gating Charge Translation Is Altered by Mutations in the Voltage Sensor Domain. <i>PLoS ONE</i> , 2012, 7, e45880.	2.5	19
16	Tracking a complete voltage-sensor cycle with metal-ion bridges. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8552-8557.	7.1	132
17	Microsecond Simulations Indicate that Ethanol Binds between Subunits and Could Stabilize an Open-State Model of a Glycine Receptor. <i>Biophysical Journal</i> , 2011, 100, 1642-1650.	0.5	72
18	Improved predictions by Pcons.net using multiple templates. <i>Bioinformatics</i> , 2011, 27, 426-427.	4.1	12

#	ARTICLE	IF	CITATIONS
19	Model quality assessment for membrane proteins. <i>Bioinformatics</i> , 2010, 26, 3067-3074.	4.1	71
20	Modeling Anesthetic Binding Sites within the Glycine Alpha One Receptor Based on Prokaryotic Ion Channel Templates: The Problem with TM4. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 2248-2255.	5.4	24
21	Prediction of membrane protein structures with complex topologies using limited constraints. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1409-1414.	7.1	140
22	Assessment of global and local model quality in CASP8 using Pcons and ProQ. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 167-172.	2.6	62
23	Using multiple templates to improve quality of homology models in automated homology modeling. <i>Protein Science</i> , 2008, 17, 990-1002.	7.6	130
24	Pcons.net: protein structure prediction meta server. <i>Nucleic Acids Research</i> , 2007, 35, W369-W374.	14.5	54
25	Prediction of global and local model quality in CASP7 using Pcons and ProQ. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 184-193.	2.6	97
26	Identification of correct regions in protein models using structural, alignment, and consensus information. <i>Protein Science</i> , 2006, 15, 900-913.	7.6	184
27	All are not equal: A benchmark of different homology modeling programs. <i>Protein Science</i> , 2005, 14, 1315-1327.	7.6	185
28	Tertiary Windowing to Detect Positive Diversifying Selection. <i>Journal of Molecular Evolution</i> , 2005, 60, 499-504.	1.8	37
29	Pcons5: combining consensus, structural evaluation and fold recognition scores. <i>Bioinformatics</i> , 2005, 21, 4248-4254.	4.1	103
30	Profile-profile methods provide improved fold-recognition: A study of different profile-profile alignment methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 188-197.	2.6	85
31	Automatic consensus-based fold recognition using Pcons, ProQ, and Pmodeller. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 534-541.	2.6	112
32	Using evolutionary information for the query and target improves fold recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 342-350.	2.6	29
33	Can correct protein models be identified?. <i>Protein Science</i> , 2003, 12, 1073-1086.	7.6	646