Björn Wallner

List of Publications by Year in descending order

		257101	395343
33 papers	**2,955** citations	**24** h-index	**33** g-index
37 all docs	**37** docs citations	**37** times ranked	**3481** citing authors

#	Article	IF	Citations
1	Can correct protein models be identified?. Protein Science, 2003, 12, 1073-1086.	3.1	646
2	DockQ: A Quality Measure for Protein-Protein Docking Models. PLoS ONE, 2016, 11, e0161879.	1.1	205
3	All are not equal: A benchmark of different homology modeling programs. Protein Science, 2005, 14, 1315-1327.	3.1	185
4	Identification of correct regions in protein models using structural, alignment, and consensus information. Protein Science, 2006, 15, 900-913.	3.1	184
5	Improved model quality assessment using ProQ2. BMC Bioinformatics, 2012, 13, 224.	1.2	173
6	Prediction of membrane protein structures with complex topologies using limited constraints. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1409-1414.	3.3	140
7	Tracking a complete voltage-sensor cycle with metal-ion bridges. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8552-8557.	3.3	132
8	Using multiple templates to improve quality of homology models in automated homology modeling. Protein Science, 2008, 17, 990-1002.	3.1	130
9	Automatic consensus-based fold recognition using Pcons, ProQ, and Pmodeller. Proteins: Structure, Function and Bioinformatics, 2003, 53, 534-541.	1.5	112
10	Pcons5: combining consensus, structural evaluation and fold recognition scores. Bioinformatics, 2005, 21, 4248-4254.	1.8	103
11	Prediction of global and local model quality in CASP7 using Pcons and ProQ. Proteins: Structure, Function and Bioinformatics, 2007, 69, 184-193.	1.5	97
12	Profile-profile methods provide improved fold-recognition: A study of different profile-profile alignment methods. Proteins: Structure, Function and Bioinformatics, 2004, 57, 188-197.	1.5	85
13	Estimation of model accuracy in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1361-1377.	1.5	78
14	Microsecond Simulations Indicate that Ethanol Binds between Subunits and Could Stabilize an Open-State Model of a Glycine Receptor. Biophysical Journal, 2011, 100, 1642-1650.	0.2	72
15	Model quality assessment for membrane proteins. Bioinformatics, 2010, 26, 3067-3074.	1.8	71
16	Assessment of global and local model quality in CASP8 using Pcons and ProQ. Proteins: Structure, Function and Bioinformatics, 2009, 77, 167-172.	1.5	62
17	rawMSA: End-to-end Deep Learning using raw Multiple Sequence Alignments. PLoS ONE, 2019, 14, e0220182.	1.1	62
18	Pcons.net: protein structure prediction meta server. Nucleic Acids Research, 2007, 35, W369-W374.	6.5	54

#	Article	IF	Citations
19	Predicting protein-peptide interaction sites using distant protein complexes as structural templates. Scientific Reports, 2019, 9, 4267.	1.6	44
20	Tertiary Windowing to Detect Positive Diversifying Selection. Journal of Molecular Evolution, 2005, 60, 499-504.	0.8	37
21	InterPred: A pipeline to identify and model protein–protein interactions. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1159-1170.	1.5	32
22	Proteus: a random forest classifier to predict disorder-to-order transitioning binding regions in intrinsically disordered proteins. Journal of Computer-Aided Molecular Design, 2017, 31, 453-466.	1.3	31
23	Charge Pair Interactions in Transmembrane Helices and Turn Propensity of the Connecting Sequence Promote Helical Hairpin Insertion. Journal of Molecular Biology, 2013, 425, 830-840.	2.0	30
24	InterPep2: global peptide–protein docking using interaction surface templates. Bioinformatics, 2020, 36, 2458-2465.	1.8	30
25	Using evolutionary information for the query and target improves fold recognition. Proteins: Structure, Function and Bioinformatics, 2003, 54, 342-350.	1.5	29
26	Methods for estimation of model accuracy in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 361-373.	1.5	27
27	Modeling Anesthetic Binding Sites within the Glycine Alpha One Receptor Based on Prokaryotic Ion Channel Templates: The Problem with TM4. Journal of Chemical Information and Modeling, 2010, 50, 2248-2255.	2.5	24
28	The Free Energy Barrier for Arginine Gating Charge Translation Is Altered by Mutations in the Voltage Sensor Domain. PLoS ONE, 2012, 7, e45880.	1.1	19
29	Improved predictions by Pcons.net using multiple templates. Bioinformatics, 2011, 27, 426-427.	1.8	12
30	Improved protein model quality assessments by changing the target function. Proteins: Structure, Function and Bioinformatics, 2018, 86, 654-663.	1.5	11
31	The MYC oncoprotein directly interacts with its chromatin cofactor PNUTS to recruit PP1 phosphatase. Nucleic Acids Research, 2022, 50, 3505-3522.	6.5	11
32	InterLig: improved ligand-based virtual screening using topologically independent structural alignments. Bioinformatics, 2020, 36, 3266-3267.	1.8	4
33	InterPepScore: a deep learning score for improving the FlexPepDock refinement protocol. Bioinformatics, 2022, 38, 3209-3215.	1.8	1