Shoshana J Wodak

List of Publications by Year
in descending order

47 papers	3,788 citations	172457 29 h-index	214800 47 g-index
70 all docs	70 docs citations	70 times ranked	4001 citing authors

#	Article	IF	Citations
1	Insight into membraneless organelles and their associated proteins: Drivers, Clients and Regulators. Computational and Structural Biotechnology Journal, 2021, 19, 3964-3977.	4.1	24
2	Integration of Data from Liquidâ€"Liquid Phase Separation Databases Highlights Concentration and Dosage Sensitivity of LLPS Drivers. International Journal of Molecular Sciences, 2021, 22, 3017.	4.1	29
3	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	2.6	73
4	Modeling proteinâ€protein, proteinâ€peptide, and proteinâ€oligosaccharide complexes: CAPRI 7th edition. Proteins: Structure, Function and Bioinformatics, 2020, 88, 916-938.	2.6	96
5	Cover Image, Volume 88, Issue 8. Proteins: Structure, Function and Bioinformatics, 2020, 88, C1.	2.6	1
6	Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. Biophysical Journal, 2020, 118, 2952-2965.	0.5	17
7	Blind prediction of homoâ€•and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
8	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. Journal of Molecular Biology, 2019, 431, 1650-1670.	4.2	41
9	The challenge of modeling protein assemblies: the CASP12â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2018, 86, 257-273.	2.6	85
10	Interplay of self-association and conformational flexibility in regulating protein function. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170190.	4.0	11
11	A benchmark testing ground for integrating homology modeling and protein docking. Proteins: Structure, Function and Bioinformatics, 2017, 85, 10-16.	2.6	29
12	Cover Image, Volume 85, Issue 3. Proteins: Structure, Function and Bioinformatics, 2017, 85, C1.	2.6	0
13	Interplay of buried histidine protonation and protein stability in prion misfolding. Scientific Reports, 2017, 7, 882.	3.3	17
14	Modeling proteinâ€"protein and proteinâ€"peptide complexes: CAPRI 6th edition. Proteins: Structure, Function and Bioinformatics, 2017, 85, 359-377.	2.6	198
15	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
16	Editorial overview: Multi-protein assemblies in signaling. Current Opinion in Structural Biology, 2016, 41, v-vii.	5.7	1
17	Computational approaches to investigating allostery. Current Opinion in Structural Biology, 2016, 41, 159-171.	5.7	63
18	Landscape of Intertwined Associations in Multi-Domain Homo-Oligomeric Proteins. Journal of Molecular Biology, 2015, 427, 350-370.	4.2	14

#	ARTICLE	IF	CITATIONS
19	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. Nature Methods, 2015, 12, 725-731.	19.0	109
20	Extracting high confidence protein interactions from affinity purification data: At the crossroads. Journal of Proteomics, 2015, 118, 63-80.	2.4	30
21	The Landscape of Intertwined Associations in Homooligomeric Proteins. Biophysical Journal, 2015, 109, 1087-1100.	0.5	17
22	Risk estimates for complex disorders: comparing personal genome testing and family history. Genetics in Medicine, 2014, 16, 231-237.	2.4	10
23	Blind prediction of interfacial water positions in CAPRI. Proteins: Structure, Function and Bioinformatics, 2014, 82, 620-632.	2.6	50
24	Intercellular network structure and regulatory motifs in the human hematopoietic system. Molecular Systems Biology, 2014, 10, 741.	7.2	57
25	Human-Chromatin-Related Protein Interactions Identify a Demethylase Complex Required for Chromosome Segregation. Cell Reports, 2014, 8, 297-310.	6.4	72
26	Protein–protein interaction networks: the puzzling riches. Current Opinion in Structural Biology, 2013, 23, 941-953.	5.7	93
27	Docking, scoring, and affinity prediction in CAPRI. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2082-2095.	2.6	216
28	Intertwined Associations in Structures of Homooligomeric Proteins. Structure, 2013, 21, 638-649.	3.3	27
29	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	2.6	87
30	Multiple Replica Repulsion Technique for Efficient Conformational Sampling of Biological Systems. Biophysical Journal, 2011, 101, 951-960.	0.5	6
31	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
32	Interaction databases on the same page. Nature Biotechnology, 2011, 29, 391-393.	17.5	36
33	High-Throughput Analyses and Curation of Protein Interactions in Yeast. Methods in Molecular Biology, 2011, 759, 381-406.	0.9	5
34	Docking and scoring protein interactions: CAPRI 2009. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3073-3084.	2.6	210
35	Blind predictions of protein interfaces by docking calculations in CAPRI. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3085-3095.	2.6	77
36	Literature curation of protein interactions: measuring agreement across major public databases. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq026-baq026.	3.0	54

#	Article	IF	Citations
37	Challenges and Rewards of Interaction Proteomics. Molecular and Cellular Proteomics, 2009, 8, 3-18.	3.8	78
38	Analysis of Genetic Interaction Maps Reveals Functional Pleiotropy. Nature Precedings, 2008, , .	0.1	0
39	Docking and scoring protein complexes: CAPRI 3rd Edition. Proteins: Structure, Function and Bioinformatics, 2007, 69, 704-718.	2.6	301
40	Assessment of CAPRI predictions in rounds 3-5 shows progress in docking procedures. Proteins: Structure, Function and Bioinformatics, 2005, 60, 150-169.	2.6	310
41	Integrative bioinformatics: making sense of the networks. Drug Discovery Today: Technologies, 2004, 1, 179-187.	4.0	3
42	Identifying structural domains in proteins. Methods of Biochemical Analysis, 2003, 44, 365-85.	0.2	3
43	Structural basis of macromolecular recognition. Advances in Protein Chemistry, 2002, 61, 9-73.	4.4	147
44	Factors Influencing the Ability of Knowledge-based Potentials to Identify Native Sequence-Structure Matches. Journal of Molecular Biology, 1994, 235, 1598-1613.	4.2	215
45	Generating and testing protein folds. Current Opinion in Structural Biology, 1993, 3, 247-259.	5.7	157
46	Extracting information on folding from the amino acid sequence: Accurate predictions for protein regions with preferred conformation in the absence of tertiary interactions. Biochemistry, 1992, 31, 10226-10238.	2.5	114
47	Prediction of protein backbone conformation based on seven structure assignments. Journal of Molecular Biology, 1991, 221, 961-979.	4.2	199