

Shoshana J Wodak

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44
papers

3,032
citations

26
h-index

55
g-index

70
ext. papers

3,433
ext. citations

6.3
avg, IF

5.37
L-index

#	Paper	IF	Citations
44	Integration of Data from Liquid-Liquid Phase Separation Databases Highlights Concentration and Dosage Sensitivity of LLPS Drivers. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	8
43	Insight into membraneless organelles and their associated proteins: Drivers, Clients and Regulators. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 3964-3977	6.8	8
42	Prediction of protein assemblies, the next frontier: The CASP14-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1800-1823	4.2	17
41	Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2020 , 118, 2952-2965	2.9	6
40	Modeling protein-protein, protein-peptide, and protein-oligosaccharide complexes: CAPRI 7th edition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 916-938	4.2	41
39	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. <i>Journal of Molecular Biology</i> , 2019 , 431, 1650-1670	6.5	24
38	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1200-1221	4.2	58
37	Interplay of self-association and conformational flexibility in regulating protein function. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018 , 373,	5.8	5
36	The challenge of modeling protein assemblies: the CASP12-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018 , 86 Suppl 1, 257-273	4.2	56
35	A benchmark testing ground for integrating homology modeling and protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, 10-16	4.2	24
34	Cover Image, Volume 85, Issue 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, C1-C1	4.2	
33	Interplay of buried histidine protonation and protein stability in prion misfolding. <i>Scientific Reports</i> , 2017 , 7, 882	4.9	14
32	Modeling protein-protein and protein-peptide complexes: CAPRI 6th edition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, 359-377	4.2	148
31	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 323-48	4.2	111
30	Computational approaches to investigating allostery. <i>Current Opinion in Structural Biology</i> , 2016 , 41, 159-171	8.1	43
29	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015 , 12, 725-31	21.6	86
28	Extracting high confidence protein interactions from affinity purification data: at the crossroads. <i>Journal of Proteomics</i> , 2015 , 118, 63-80	3.9	19

27	The Landscape of Intertwined Associations in Homooligomeric Proteins. <i>Biophysical Journal</i> , 2015 , 109, 1087-100	2.9	11
26	Landscape of intertwined associations in multi-domain homo-oligomeric proteins. <i>Journal of Molecular Biology</i> , 2015 , 427, 350-70	6.5	11
25	Blind prediction of interfacial water positions in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 620-32	4.2	43
24	Intercellular network structure and regulatory motifs in the human hematopoietic system. <i>Molecular Systems Biology</i> , 2014 , 10, 741	12.2	41
23	Human-chromatin-related protein interactions identify a demethylase complex required for chromosome segregation. <i>Cell Reports</i> , 2014 , 8, 297-310	10.6	46
22	Risk estimates for complex disorders: comparing personal genome testing and family history. <i>Genetics in Medicine</i> , 2014 , 16, 231-7	8.1	9
21	Protein-protein interaction networks: the puzzling riches. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 941-53	8.1	65
20	Docking, scoring, and affinity prediction in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 2082-95	4.2	186
19	Intertwined associations in structures of homooligomeric proteins. <i>Structure</i> , 2013 , 21, 638-49	5.2	23
18	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 1980-7	4.2	78
17	Multiple replica repulsion technique for efficient conformational sampling of biological systems. <i>Biophysical Journal</i> , 2011 , 101, 951-60	2.9	6
16	Community-wide assessment of protein-interface modeling suggests improvements to design methodology. <i>Journal of Molecular Biology</i> , 2011 , 414, 289-302	6.5	114
15	Interaction databases on the same page. <i>Nature Biotechnology</i> , 2011 , 29, 391-3	44.5	33
14	High-throughput analyses and curation of protein interactions in yeast. <i>Methods in Molecular Biology</i> , 2011 , 759, 381-406	1.4	5
13	Literature curation of protein interactions: measuring agreement across major public databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2010 , 2010, baq026	5	48
12	Docking and scoring protein interactions: CAPRI 2009. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 3073-84	4.2	190
11	Blind predictions of protein interfaces by docking calculations in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 3085-95	4.2	68
10	Challenges and rewards of interaction proteomics. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 3-18	7.6	72

9	Docking and scoring protein complexes: CAPRI 3rd Edition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 704-18	4.2	254
8	Assessment of CAPRI predictions in rounds 3-5 shows progress in docking procedures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 150-69	4.2	281
7	Integrative bioinformatics: making sense of the networks. <i>Drug Discovery Today: Technologies</i> , 2004 , 1, 179-87	7.1	3
6	Identifying structural domains in proteins. <i>Methods of Biochemical Analysis</i> , 2003 , 44, 365-85		3
5	Structural basis of macromolecular recognition. <i>Advances in Protein Chemistry</i> , 2002 , 61, 9-73		126
4	Factors influencing the ability of knowledge-based potentials to identify native sequence-structure matches. <i>Journal of Molecular Biology</i> , 1994 , 235, 1598-613	6.5	196
3	Generating and testing protein folds. <i>Current Opinion in Structural Biology</i> , 1993 , 3, 247-259	8.1	144
2	Extracting information on folding from the amino acid sequence: accurate predictions for protein regions with preferred conformation in the absence of tertiary interactions. <i>Biochemistry</i> , 1992 , 31, 10226-38	3.2	106
1	Prediction of protein backbone conformation based on seven structure assignments. Influence of local interactions. <i>Journal of Molecular Biology</i> , 1991 , 221, 961-79	6.5	180