

Shoshana J Wodak

List of Publications by Citations

Source: <https://exaly.com/author-pdf/2730747/shoshana-j-wodak-publications-by-citations.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
43	Docking and scoring protein complexes: CAPRI 3rd Edition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 704-18	4.2	254
42	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
41	Docking and scoring protein interactions: CAPRI 2009. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 3073-84	4.2	190
40	Docking, scoring, and affinity prediction in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 2082-95	4.2	186
39	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
38	Modeling protein-protein and protein-peptide complexes: CAPRI 6th edition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, 359-377	4.2	148
37	Generating and testing protein folds. <i>Current Opinion in Structural Biology</i> , 1993 , 3, 247-259	8.1	144
36	Structural basis of macromolecular recognition. <i>Advances in Protein Chemistry</i> , 2002 , 61, 9-73		126
35	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
34	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
33	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
32	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
31	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
30	Challenges and rewards of interaction proteomics. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 3-18	7.6	72
29	Blind predictions of protein interfaces by docking calculations in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 3085-95	4.2	68
28	Protein-protein interaction networks: the puzzling riches. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 941-53	8.1	65

27	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
26	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
25	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
24	Human-chromatin-related protein interactions identify a demethylase complex required for chromosome segregation. <i>Cell Reports</i> , 2014 , 8, 297-310	10.6	46
23	Blind prediction of interfacial water positions in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 620-32	4.2	43
22	Computational approaches to investigating allostery. <i>Current Opinion in Structural Biology</i> , 2016 , 41, 159-171	8.1	43
21	Intercellular network structure and regulatory motifs in the human hematopoietic system. <i>Molecular Systems Biology</i> , 2014 , 10, 741	12.2	41
20	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
19	Interaction databases on the same page. <i>Nature Biotechnology</i> , 2011 , 29, 391-3	44.5	33
18	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
17	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
16	Intertwined associations in structures of homooligomeric proteins. <i>Structure</i> , 2013 , 21, 638-49	5.2	23
15	Extracting high confidence protein interactions from affinity purification data: at the crossroads. <i>Journal of Proteomics</i> , 2015 , 118, 63-80	3.9	19
14	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
13	Interplay of buried histidine protonation and protein stability in prion misfolding. <i>Scientific Reports</i> , 2017 , 7, 882	4.9	14
12	The Landscape of Intertwined Associations in Homooligomeric Proteins. <i>Biophysical Journal</i> , 2015 , 109, 1087-100	2.9	11
11	Landscape of intertwined associations in multi-domain homo-oligomeric proteins. <i>Journal of Molecular Biology</i> , 2015 , 427, 350-70	6.5	11
10	Risk estimates for complex disorders: comparing personal genome testing and family history. <i>Genetics in Medicine</i> , 2014 , 16, 231-7	8.1	9

9	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
8	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
7	Multiple replica repulsion technique for efficient conformational sampling of biological systems. <i>Biophysical Journal</i> , 2011 , 101, 951-60	2.9	6
6	Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2020 , 118, 2952-2965	2.9	6
5	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
4	High-throughput analyses and curation of protein interactions in yeast. <i>Methods in Molecular Biology</i> , 2011 , 759, 381-406	1.4	5
3	Integrative bioinformatics: making sense of the networks. <i>Drug Discovery Today: Technologies</i> , 2004 , 1, 179-87	7.1	3
2	Identifying structural domains in proteins. <i>Methods of Biochemical Analysis</i> , 2003 , 44, 365-85		3
1	Cover Image, Volume 85, Issue 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, C1-C1	4.2	