

Shoshana J Wodak

List of Publications by Year in descending order

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Version: 2024-02-01

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	Assessment of CAPRI predictions in rounds 3-5 shows progress in docking procedures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 150-169.	2.6	310
2	Docking and scoring protein complexes: CAPRI 3rd Edition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 704-718.	2.6	301
3	Docking, scoring, and affinity prediction in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2082-2095.	2.6	216
4	Factors Influencing the Ability of Knowledge-based Potentials to Identify Native Sequence-Structure Matches. <i>Journal of Molecular Biology</i> , 1994, 235, 1598-1613.	4.2	215
5	Docking and scoring protein interactions: CAPRI 2009. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3073-3084.	2.6	210
6	Prediction of protein backbone conformation based on seven structure assignments. <i>Journal of Molecular Biology</i> , 1991, 221, 961-979.	4.2	199
7	Modeling protein-protein and protein-peptide complexes: CAPRI 6th edition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 359-377.	2.6	198
8	Generating and testing protein folds. <i>Current Opinion in Structural Biology</i> , 1993, 3, 247-259.	5.7	157
9	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, 323-348.	2.6	148
10	Structural basis of macromolecular recognition. <i>Advances in Protein Chemistry</i> , 2002, 61, 9-73.	4.4	147
11	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	4.2	131
12	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, 10226-10238.	2.5	114
13	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015, 12, 725-731.	19.0	109
14	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	2.6	99
15	Modeling protein-protein, protein-peptide, and protein-oligosaccharide complexes: CAPRI 7th edition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 916-938.	2.6	96
16	Protein-protein interaction networks: the puzzling riches. <i>Current Opinion in Structural Biology</i> , 2013, 23, 941-953.	5.7	93
17	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1980-1987.	2.6	87
18	The challenge of modeling protein assemblies: the CASP12-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 257-273.	2.6	85

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19	Challenges and Rewards of Interaction Proteomics. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 3-18.	3.8	78
20	Blind predictions of protein interfaces by docking calculations in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3085-3095.	2.6	77
21	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1800-1823.	2.6	73
22	Human-Chromatin-Related Protein Interactions Identify a Demethylase Complex Required for Chromosome Segregation. <i>Cell Reports</i> , 2014, 8, 297-310.	6.4	72
23	Computational approaches to investigating allostery. <i>Current Opinion in Structural Biology</i> , 2016, 41, 159-171.	5.7	63
24	Intercellular network structure and regulatory motifs in the human hematopoietic system. <i>Molecular Systems Biology</i> , 2014, 10, 741.	7.2	57
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-baq026.	3.0	54
26	Blind prediction of interfacial water positions in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 620-632.	2.6	50
27	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. <i>Journal of Molecular Biology</i> , 2019, 431, 1650-1670.	4.2	41
28	Interaction databases on the same page. <i>Nature Biotechnology</i> , 2011, 29, 391-393.	17.5	36
29	Extracting high confidence protein interactions from affinity purification data: At the crossroads. <i>Journal of Proteomics</i> , 2015, 118, 63-80.	2.4	30
30	A benchmark testing ground for integrating homology modeling and protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 10-16.	2.6	29
31	Integration of Data from Liquidâ€Liquid Phase Separation Databases Highlights Concentration and Dosage Sensitivity of LLPS Drivers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3017.	4.1	29
32	Intertwined Associations in Structures of Homooligomeric Proteins. <i>Structure</i> , 2013, 21, 638-649.	3.3	27
33	Insight into membraneless organelles and their associated proteins: Drivers, Clients and Regulators. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3964-3977.	4.1	24
34	The Landscape of Intertwined Associations in Homooligomeric Proteins. <i>Biophysical Journal</i> , 2015, 109, 1087-1100.	0.5	17
35	Interplay of buried histidine protonation and protein stability in prion misfolding. <i>Scientific Reports</i> , 2017, 7, 882.	3.3	17
36	Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2020, 118, 2952-2965.	0.5	17

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37	Landscape of Intertwined Associations in Multi-Domain Homo-Oligomeric Proteins. <i>Journal of Molecular Biology</i> , 2015, 427, 350-370.	4.2	14
38	Interplay of self-association and conformational flexibility in regulating protein function. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170190.	4.0	11
39	Risk estimates for complex disorders: comparing personal genome testing and family history. <i>Genetics in Medicine</i> , 2014, 16, 231-237.	2.4	10
40	Multiple Replica Repulsion Technique for Efficient Conformational Sampling of Biological Systems. <i>Biophysical Journal</i> , 2011, 101, 951-960.	0.5	6
41	High-Throughput Analyses and Curation of Protein Interactions in Yeast. <i>Methods in Molecular Biology</i> , 2011, 759, 381-406.	0.9	5
42	Integrative bioinformatics: making sense of the networks. <i>Drug Discovery Today: Technologies</i> , 2004, 1, 179-187.	4.0	3
43	Identifying structural domains in proteins. <i>Methods of Biochemical Analysis</i> , 2003, 44, 365-85.	0.2	3
44	Editorial overview: Multi-protein assemblies in signaling. <i>Current Opinion in Structural Biology</i> , 2016, 41, v-vii.	5.7	1
45	Cover Image, Volume 88, Issue 8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, C1.	2.6	1
46	Analysis of Genetic Interaction Maps Reveals Functional Pleiotropy. <i>Nature Precedings</i> , 2008, , .	0.1	0
47	Cover Image, Volume 85, Issue 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C1.	2.6	0