

Ora Schueler-Furman

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101
papers

5,679
citations

40
h-index

75
g-index

112
ext. papers

7,052
ext. citations

6.8
avg, IF

5.62
L-index

#	Paper	IF	Citations
101	Protein-protein docking with simultaneous optimization of rigid-body displacement and side-chain conformations. <i>Journal of Molecular Biology</i> , 2003 , 331, 281-99	6.5	858
100	The structural basis of peptide-protein binding strategies. <i>Structure</i> , 2010 , 18, 188-99	5.2	302
99	Rosetta FlexPepDock web server--high resolution modeling of peptide-protein interactions. <i>Nucleic Acids Research</i> , 2011 , 39, W249-53	20.1	273
98	Sub-angstrom modeling of complexes between flexible peptides and globular proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 2029-40	4.2	273
97	Progress in modeling of protein structures and interactions. <i>Science</i> , 2005 , 310, 638-42	33.3	244
96	Rosetta FlexPepDock ab-initio: simultaneous folding, docking and refinement of peptides onto their receptors. <i>PLoS ONE</i> , 2011 , 6, e18934	3.7	193
95	Improved side-chain modeling for protein-protein docking. <i>Protein Science</i> , 2005 , 14, 1328-39	6.3	182
94	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020 , 17, 665-680	21.6	165
93	Druggable protein-protein interactions--from hot spots to hot segments. <i>Current Opinion in Chemical Biology</i> , 2013 , 17, 952-9	9.7	160
92	Rosetta predictions in CASP5: successes, failures, and prospects for complete automation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 457-68	4.2	142
91	Structure-based prediction of binding peptides to MHC class I molecules: application to a broad range of MHC alleles. <i>Protein Science</i> , 2000 , 9, 1838-46	6.3	133
90	Can self-inhibitory peptides be derived from the interfaces of globular protein-protein interactions?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 3140-9	4.2	124
89	Protein-peptide docking: opportunities and challenges. <i>Drug Discovery Today</i> , 2018 , 23, 1530-1537	8.8	118
88	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
87	Application of asymmetric statistical potentials to antibody-protein docking. <i>Bioinformatics</i> , 2012 , 28, 2608-14	7.2	108
86	Relacin, a novel antibacterial agent targeting the Stringent Response. <i>PLoS Pathogens</i> , 2012 , 8, e1002925	5.6	105
85	Protein-protein docking predictions for the CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 118-22	4.2	93

84	Progress in protein-protein docking: atomic resolution predictions in the CAPRI experiment using RosettaDock with an improved treatment of side-chain flexibility. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 187-94	4.2	87
83	Folding of the C-terminal bacterial binding domain in statherin upon adsorption onto hydroxyapatite crystals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 16083-8	11.5	84
82	The Escherichia coli extracellular death factor EDF induces the endoribonucleolytic activities of the toxins MazF and ChpBK. <i>Molecular Cell</i> , 2011 , 41, 625-35	17.6	82
81	Ubiquitination and degradation of the inhibitors of NF-kappaB. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010 , 2, a000166	10.2	80
80	Learning MHC I-peptide binding. <i>Bioinformatics</i> , 2006 , 22, e227-35	7.2	74
79	Peptide docking and structure-based characterization of peptide binding: from knowledge to know-how. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 894-902	8.1	72
78	Detection of peptide-binding sites on protein surfaces: the first step toward the modeling and targeting of peptide-mediated interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 2096-105	4.2	71
77	Fractured genes: a novel genomic arrangement involving new split inteins and a new homing endonuclease family. <i>Nucleic Acids Research</i> , 2009 , 37, 2560-73	20.1	68
76	High-resolution global peptide-protein docking using fragments-based PIPER-FlexPepDock. <i>PLoS Computational Biology</i> , 2017 , 13, e1005905	5	58
75	Mitochondrial complex IV deficiency, caused by mutated COX6B1, is associated with encephalomyopathy, hydrocephalus and cardiomyopathy. <i>European Journal of Human Genetics</i> , 2015 , 23, 159-64	5.3	58
74	ClusPro PeptiDock: efficient global docking of peptide recognition motifs using FFT. <i>Bioinformatics</i> , 2017 , 33, 3299-3301	7.2	54
73	Conserved residue clustering and protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 225-35	4.2	53
72	A model of anthrax toxin lethal factor bound to protective antigen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 16409-14	11.5	52
71	Peptiderive server: derive peptide inhibitors from protein-protein interactions. <i>Nucleic Acids Research</i> , 2016 , 44, W536-41	20.1	49
70	Rapid sampling of molecular motions with prior information constraints. <i>PLoS Computational Biology</i> , 2009 , 5, e1000295	5	46
69	Identification of a novel class of farnesylation targets by structure-based modeling of binding specificity. <i>PLoS Computational Biology</i> , 2011 , 7, e1002170	5	46
68	Trans protein splicing of cyanobacterial split inteins in endogenous and exogenous combinations. <i>Biochemistry</i> , 2007 , 46, 322-30	3.2	45
67	Is GAS1 a co-receptor for the GDNF family of ligands?. <i>Trends in Pharmacological Sciences</i> , 2006 , 27, 72-7	13.2	43

66	Computational approaches to investigating allostery. <i>Current Opinion in Structural Biology</i> , 2016 , 41, 159-171	8.1	43
65	Encounter complexes and dimensionality reduction in protein-protein association. <i>ELife</i> , 2014 , 3, e013708.9		42
64	Pathogens use structural mimicry of native host ligands as a mechanism for host receptor engagement. <i>Cell Host and Microbe</i> , 2013 , 14, 63-73	23.4	41
63	Pleiotropic Functions of Tumor Suppressor WWOX in Normal and Cancer Cells. <i>Journal of Biological Chemistry</i> , 2015 , 290, 30728-35	5.4	41
62	The structure, dynamics, and energetics of protein adsorption-lessons learned from adsorption of statherin to hydroxyapatite. <i>Magnetic Resonance in Chemistry</i> , 2007 , 45 Suppl 1, S32-47	2.1	41
61	Knowledge-based structure prediction of MHC class I bound peptides: a study of 23 complexes. <i>Folding & Design</i> , 1998 , 3, 549-64		40
60	Myelin-associated glycoprotein gene mutation causes Pelizaeus-Merzbacher disease-like disorder. <i>Brain</i> , 2015 , 138, 2521-36	11.2	37
59	Discrimination of near-native structures in protein-protein docking by testing the stability of local minima. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 72, 993-1004	4.2	36
58	Structure-Based Identification of HDAC8 Non-histone Substrates. <i>Structure</i> , 2016 , 24, 458-68	5.2	31
57	In silico and in vitro elucidation of BH3 binding specificity toward Bcl-2. <i>Biochemistry</i> , 2012 , 51, 5841-50	3.2	30
56	Minimizing and learning energy functions for side-chain prediction. <i>Journal of Computational Biology</i> , 2008 , 15, 899-911	1.7	30
55	Funnel hunting in a rough terrain: learning and discriminating native energy funnels. <i>Structure</i> , 2008 , 16, 269-79	5.2	27
54	RosettaDock in CAPRI rounds 6-12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 758-63	4.2	26
53	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
52	Anchoring of bacterial effectors to host membranes through host-mediated lipidation by prenylation: a common paradigm. <i>Trends in Microbiology</i> , 2011 , 19, 573-9	12.4	24
51	Identifying a common molecular mechanism for inhibition of MITF and STAT3 by PIAS3. <i>Blood</i> , 2006 , 107, 2839-45	2.2	24
50	Modeling Peptide-Protein Structure and Binding Using Monte Carlo Sampling Approaches: Rosetta FlexPepDock and FlexPepBind. <i>Methods in Molecular Biology</i> , 2017 , 1561, 139-169	1.4	22
49	c-Abl phosphorylates E6AP and regulates its E3 ubiquitin ligase activity. <i>Biochemistry</i> , 2013 , 52, 3119-29	3.2	22

48	Autophosphorylation activates Dictyostelium myosin II heavy chain kinase A by providing a ligand for an allosteric binding site in the alpha-kinase domain. <i>Journal of Biological Chemistry</i> , 2011 , 286, 2607-16	5.4	22
47	Versatile communication strategies among tandem WW domain repeats. <i>Experimental Biology and Medicine</i> , 2015 , 240, 351-60	3.7	21
46	Extending RosettaDock with water, sugar, and pH for prediction of complex structures and affinities for CAPRI rounds 20-27. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 2201-9	4.2	20
45	Parkin Somatic Mutations Link Melanoma and Parkinson's Disease. <i>Journal of Genetics and Genomics</i> , 2016 , 43, 369-79	4	19
44	is associated with recessive primary familial brain calcification. <i>Annals of Clinical and Translational Neurology</i> , 2019 , 6, 106-113	5.3	19
43	Harnessing protein folding neural networks for peptide-protein docking.. <i>Nature Communications</i> , 2022 , 13, 176	17.4	18
42	FlexPepDock lessons from CAPRI peptide-protein rounds and suggested new criteria for assessment of model quality and utility. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, 445-462	4.2	15
41	Better together: Elements of successful scientific software development in a distributed collaborative community. <i>PLoS Computational Biology</i> , 2020 , 16, e1007507	5	15
40	FunHunt: model selection based on energy landscape characteristics. <i>Biochemical Society Transactions</i> , 2008 , 36, 1418-21	5.1	15
39	Examination of possible structural constraints of MHC-binding peptides by assessment of their native structure within their source proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 45, 47-54	4.2	15
38	Assessing the energy landscape of CAPRI targets by FunHunt. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 809-15	4.2	14
37	Rationally Designed Macrocyclic Peptides as Synergistic Agonists of LPS-Induced Inflammatory Response. <i>Tetrahedron</i> , 2014 , 70, 7664-7668	2.4	13
36	Modeling peptide-protein interactions. <i>Methods in Molecular Biology</i> , 2012 , 857, 375-98	1.4	13
35	The SV40 capsid is stabilized by a conserved pentapeptide hinge of the major capsid protein VP1. <i>Journal of Molecular Biology</i> , 2009 , 386, 1382-91	6.5	13
34	Crucial roles of single residues in binding affinity, specificity, and promiscuity in the cellulosomal cohesin-dockerin interface. <i>Journal of Biological Chemistry</i> , 2015 , 290, 13654-66	5.4	12
33	Escherichia coli Quorum-Sensing EDF, A Peptide Generated by Novel Multiple Distinct Mechanisms and Regulated by trans-Translation. <i>MBio</i> , 2016 , 7, e02034-15	7.8	12
32	Harnessing protein folding neural networks for peptide-protein docking		11
31	Indirect ELISA-based approach for comparative measurement of high-affinity cohesin-dockerin interactions. <i>Journal of Molecular Recognition</i> , 2012 , 25, 616-22	2.6	10

30	Evolving dual targeting of a prokaryotic protein in yeast. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1563-1573	10
29	On the use of structural templates for high-resolution docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 1939-49	4.2 10
28	Novel Structural Mechanism of Allosteric Regulation of Aspartic Peptidases via an Evolutionarily Conserved Exosite. <i>Cell Chemical Biology</i> , 2018 , 25, 318-329.e4	8.2 9
27	Yeast aconitase mitochondrial import is modulated by interactions of its C and N terminal domains and Ssa1/2 (Hsp70). <i>Scientific Reports</i> , 2018 , 8, 5903	4.9 8
26	Host FIH-Mediated Asparaginyl Hydroxylation of Translocated Effectors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017 , 7, 54	5.9 8
25	Modeling beta-sheet peptide-protein interactions: Rosetta FlexPepDock in CAPRI rounds 38-45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 1037-1049	4.2 8
24	Molecular pathogenesis of human CD59 deficiency. <i>Neurology: Genetics</i> , 2018 , 4, e280	3.8 8
23	Increased sequence conservation of domain repeats in prokaryotic proteins. <i>Trends in Genetics</i> , 2010 , 26, 383-7	8.5 7
22	Detection of Peptide-Binding Sites on Protein Surfaces Using the Peptimap Server. <i>Methods in Molecular Biology</i> , 2017 , 1561, 11-20	1.4 5
21	Measurements of relative binding of cohesin and dockerin mutants using an advanced ELISA technique for high-affinity interactions. <i>Methods in Enzymology</i> , 2012 , 510, 417-28	1.7 4
20	Minimizing and Learning Energy Functions for Side-Chain Prediction 2007 , 381-395	4
19	CladeOScope: functional interactions through the prism of clade-wise co-evolution. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab024	3.7 4
18	Protocols for All-Atom Reconstruction and High-Resolution Refinement of Protein-Peptide Complex Structures. <i>Methods in Molecular Biology</i> , 2020 , 2165, 273-287	1.4 4
17	Phosphorylation of the WWOX Protein Regulates Its Interaction with p73. <i>ChemBioChem</i> , 2020 , 21, 1843-1851	3.8 3
16	ClusPro in rounds 38 to 45 of CAPRI: Toward combining template-based methods with free docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 1082-1090	4.2 3
15	A unique -associated variant in a Georgian Jewish family with probable North Carolina macular dystrophy and the possible contribution of a unique variant. <i>Molecular Vision</i> , 2020 , 26, 299-310	2.3 3
14	High-resolution global peptide-protein docking using fragments-based PIPER-FlexPepDock	2
13	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks	2

12	Harnessing protein folding neural networks for peptide-protein docking		2
11	Matching protein surface structural patches for high-resolution blind peptide docking.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2121153119	11.5	2
10	Structure-based prediction of HDAC6 substrates validated by enzymatic assay reveals determinants of promiscuity and detects new potential substrates.. <i>Scientific Reports</i> , 2022 , 12, 1788	4.9	1
9	Defining binding motifs and dynamics of the multi-pocket FERM domain from ezrin, radixin, moesin and merlin		1
8	Structure-based prediction of KDAC6 substrates validated by enzymatic assay reveals determinants of promiscuity and detects new potential substrates		1
7	PatchMAN docking: Modeling peptide-protein interactions in the context of the receptor surface		1
6	Structural basis for UFM1 transfer from UBA5 to UFC1. <i>Nature Communications</i> , 2021 , 12, 5708	17.4	1
5	Targeting an Interaction Between Two Disordered Domains by Using a Designed Peptide. <i>Chemistry - A European Journal</i> , 2020 , 26, 10240-10249	4.8	0
4	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , 2021 , 12, 6947	17.4	0
3	High-resolution Protein-Protein Docking 2010 , 209-235		
2	Targeting an Interaction Between Two Disordered Domains by Using a Designed Peptide. <i>Chemistry - A European Journal</i> , 2020 , 26, 10156	4.8	
1	Multi-system neurological disorder associated with a CRYAB variant. <i>Neurogenetics</i> , 2021 , 22, 117-125		3