Ora Schueler-Furman

List of Publications by Year in Descending Order

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	Structure-based prediction of HDAC6 substrates validated by enzymatic assay reveals determinants of promiscuity and detects new potential substrates.. *Scientific Reports*, **2022**, 12, 1788	4.9	1
100	Harnessing protein folding neural networks for peptide-protein docking.. *Nature Communications*, **2022**, 13, 176	17.4	18
99	Matching protein surface structural patches for high-resolution blind peptide docking.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119, e2121153119	11.5	2
98	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. *Nature Communications*, **2021**, 12, 6947	17.4	0
97	Multi-system neurological disorder associated with a CRYAB variant. *Neurogenetics*, **2021**, 22, 117-125	3	
96	CladeOScope: functional interactions through the prism of clade-wise co-evolution. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab024	3.7	4
95	Structural basis for UFM1 transfer from UBA5 to UFC1. *Nature Communications*, **2021**, 12, 5708	17.4	1
94	Better together: Elements of successful scientific software development in a distributed collaborative community. *PLoS Computational Biology*, **2020**, 16, e1007507	5	15
93	Macromolecular modeling and design in Rosetta: recent methods and frameworks. *Nature Methods*, **2020**, 17, 665-680	21.6	165
92	Targeting an Interaction Between Two Disordered Domains by Using a Designed Peptide. *Chemistry - A European Journal*, **2020**, 26, 10240-10249	4.8	0
91	Phosphorylation of the WWOX Protein Regulates Its Interaction with p73. *ChemBioChem*, **2020**, 21, 1843-1851	3.8	3
90	ClusPro in rounds 38 to 45 of CAPRI: Toward combining template-based methods with free docking. *Proteins: Structure, Function and Bioinformatics*, **2020**, 88, 1082-1090	4.2	3
89	A unique -associated variant in a Georgian Jewish family with probable North Carolina macular dystrophy and the possible contribution of a unique variant. *Molecular Vision*, **2020**, 26, 299-310	2.3	3
88	Modeling beta-sheet peptide-protein interactions: Rosetta FlexPepDock in CAPRI rounds 38-45. *Proteins: Structure, Function and Bioinformatics*, **2020**, 88, 1037-1049	4.2	8
87	Targeting an Interaction Between Two Disordered Domains by Using a Designed Peptide. *Chemistry - A European Journal*, **2020**, 26, 10156	4.8	
86	Protocols for All-Atom Reconstruction and High-Resolution Refinement of Protein-Peptide Complex Structures. *Methods in Molecular Biology*, **2020**, 2165, 273-287	1.4	4
85	is associated with recessive primary familial brain calcification. *Annals of Clinical and Translational Neurology*, **2019**, 6, 106-113	5.3	19

84	Yeast aconitase mitochondrial import is modulated by interactions of its C and N terminal domains and Ssa1/2 (Hsp70). *Scientific Reports*, **2018**, 8, 5903	4.9	8
83	Novel Structural Mechanism of Allosteric Regulation of Aspartic Peptidases via an Evolutionarily Conserved Exosite. *Cell Chemical Biology*, **2018**, 25, 318-329.e4	8.2	9
82	Protein-peptide docking: opportunities and challenges. *Drug Discovery Today*, **2018**, 23, 1530-1537	8.8	118
81	Molecular pathogenesis of human CD59 deficiency. *Neurology: Genetics*, **2018**, 4, e280	3.8	8
80	A benchmark testing ground for integrating homology modeling and protein docking. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 10-16	4.2	24
79	Modeling Peptide-Protein Structure and Binding Using Monte Carlo Sampling Approaches: Rosetta FlexPepDock and FlexPepBind. *Methods in Molecular Biology*, **2017**, 1561, 139-169	1.4	22
78	ClusPro PeptiDock: efficient global docking of peptide recognition motifs using FFT. *Bioinformatics*, **2017**, 33, 3299-3301	7.2	54
77	FlexPepDock lessons from CAPRI peptide-protein rounds and suggested new criteria for assessment of model quality and utility. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 445-462	4.2	15
76	High-resolution global peptide-protein docking using fragments-based PIPER-FlexPepDock. *PLoS Computational Biology*, **2017**, 13, e1005905	5	58
75	Host FIH-Mediated Asparaginyl Hydroxylation of Translocated Effectors. *Frontiers in Cellular and Infection Microbiology*, **2017**, 7, 54	5.9	8
74	Detection of Peptide-Binding Sites on Protein Surfaces Using the Peptimap Server. *Methods in Molecular Biology*, **2017**, 1561, 11-20	1.4	5
73	Parkin Somatic Mutations Link Melanoma and Parkinson's Disease. *Journal of Genetics and Genomics* , **2016**, 43, 369-79	4	19
72	Structure-Based Identification of HDAC8 Non-histone Substrates. *Structure*, **2016**, 24, 458-68	5.2	31
71	Escherichia coli Quorum-Sensing EDF, A Peptide Generated by Novel Multiple Distinct Mechanisms and Regulated by trans-Translation. *MBio*, **2016**, 7, e02034-15	7.8	12
70	Peptiderive server: derive peptide inhibitors from protein-protein interactions. *Nucleic Acids Research*, **2016**, 44, W536-41	20.1	49
69	Computational approaches to investigating allostery. *Current Opinion in Structural Biology*, **2016**, 41, 159-171	8.1	43
68	Versatile communication strategies among tandem WW domain repeats. *Experimental Biology and Medicine*, **2015**, 240, 351-60	3.7	21
67	Myelin-associated glycoprotein gene mutation causes Pelizaeus-Merzbacher disease-like disorder. *Brain*, **2015**, 138, 2521-36	11.2	37

66	Crucial roles of single residues in binding affinity, specificity, and promiscuity in the cellulosomal cohesin-dockerin interface. *Journal of Biological Chemistry*, **2015**, 290, 13654-66	5.4	12
65	Pleiotropic Functions of Tumor Suppressor WWOX in Normal and Cancer Cells. *Journal of Biological Chemistry*, **2015**, 290, 30728-35	5.4	41
64	Mitochondrial complex IV deficiency, caused by mutated COX6B1, is associated with encephalomyopathy, hydrocephalus and cardiomyopathy. *European Journal of Human Genetics*, **2015**, 23, 159-64	5.3	58
63	Rationally Designed Macrocyclic Peptides as Synergistic Agonists of LPS-Induced Inflammatory Response. *Tetrahedron*, **2014**, 70, 7664-7668	2.4	13
62	Encounter complexes and dimensionality reduction in protein-protein association. *ELife*, **2014**, 3, e01370	8.9	42
61	Pathogens use structural mimicry of native host ligands as a mechanism for host receptor engagement. *Cell Host and Microbe*, **2013**, 14, 63-73	23.4	41
60	Druggable protein-protein interactions--from hot spots to hot segments. *Current Opinion in Chemical Biology*, **2013**, 17, 952-9	9.7	160
59	Peptide docking and structure-based characterization of peptide binding: from knowledge to know-how. *Current Opinion in Structural Biology*, **2013**, 23, 894-902	8.1	72
58	Detection of peptide-binding sites on protein surfaces: the first step toward the modeling and targeting of peptide-mediated interactions. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 2096-105	4.2	71
57	c-Abl phosphorylates E6AP and regulates its E3 ubiquitin ligase activity. *Biochemistry*, **2013**, 52, 3119-29	3.2	22
56	Evolving dual targeting of a prokaryotic protein in yeast. *Molecular Biology and Evolution*, **2013**, 30, 1563-73	8.3	10
55	Extending RosettaDock with water, sugar, and pH for prediction of complex structures and affinities for CAPRI rounds 20-27. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 2201-9	4.2	20
54	Indirect ELISA-based approach for comparative measurement of high-affinity cohesin-dockerin interactions. *Journal of Molecular Recognition*, **2012**, 25, 616-22	2.6	10
53	In silico and in vitro elucidation of BH3 binding specificity toward Bcl-2. *Biochemistry*, **2012**, 51, 5841-50	3.2	30
52	Measurements of relative binding of cohesin and dockerin mutants using an advanced ELISA technique for high-affinity interactions. *Methods in Enzymology*, **2012**, 510, 417-28	1.7	4
51	Modeling peptide-protein interactions. *Methods in Molecular Biology*, **2012**, 857, 375-98	1.4	13
50	Relacin, a novel antibacterial agent targeting the Stringent Response. *PLoS Pathogens*, **2012**, 8, e1002925	7.6	105
49	Application of asymmetric statistical potentials to antibody-protein docking. *Bioinformatics*, **2012**, 28, 2608-14	7.2	108

48	The Escherichia coli extracellular death factor EDF induces the endoribonucleolytic activities of the toxins MazF and ChpBK. *Molecular Cell*, **2011**, 41, 625-35	17.6	82
47	Community-wide assessment of protein-interface modeling suggests improvements to design methodology. *Journal of Molecular Biology*, **2011**, 414, 289-302	6.5	114
46	Anchoring of bacterial effectors to host membranes through host-mediated lipidation by prenylation: a common paradigm. *Trends in Microbiology*, **2011**, 19, 573-9	12.4	24
45	Rosetta FlexPepDock web server--high resolution modeling of peptide-protein interactions. *Nucleic Acids Research*, **2011**, 39, W249-53	20.1	273
44	Autophosphorylation activates Dictyostelium myosin II heavy chain kinase A by providing a ligand for an allosteric binding site in the alpha-kinase domain. *Journal of Biological Chemistry*, **2011**, 286, 2607-16	5.4	22
43	Identification of a novel class of farnesylation targets by structure-based modeling of binding specificity. *PLoS Computational Biology*, **2011**, 7, e1002170	5	46
42	Rosetta FlexPepDock ab-initio: simultaneous folding, docking and refinement of peptides onto their receptors. *PLoS ONE*, **2011**, 6, e18934	3.7	193
41	Ubiquitination and degradation of the inhibitors of NF-kappaB. *Cold Spring Harbor Perspectives in Biology*, **2010**, 2, a000166	10.2	80
40	High-resolution Protein-Protein Docking **2010**, 209-235		
39	The structural basis of peptide-protein binding strategies. *Structure*, **2010**, 18, 188-99	5.2	302
38	Increased sequence conservation of domain repeats in prokaryotic proteins. *Trends in Genetics*, **2010**, 26, 383-7	8.5	7
37	On the use of structural templates for high-resolution docking. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 1939-49	4.2	10
36	Sub-angstrom modeling of complexes between flexible peptides and globular proteins. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 2029-40	4.2	273
35	Can self-inhibitory peptides be derived from the interfaces of globular protein-protein interactions?. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 3140-9	4.2	124
34	Rapid sampling of molecular motions with prior information constraints. *PLoS Computational Biology*, **2009**, 5, e1000295	5	46
33	Fractured genes: a novel genomic arrangement involving new split inteins and a new homing endonuclease family. *Nucleic Acids Research*, **2009**, 37, 2560-73	20.1	68
32	The SV40 capsid is stabilized by a conserved pentapeptide hinge of the major capsid protein VP1. *Journal of Molecular Biology*, **2009**, 386, 1382-91	6.5	13
31	Funnel hunting in a rough terrain: learning and discriminating native energy funnels. *Structure*, **2008**, 16, 269-79	5.2	27

30	Minimizing and learning energy functions for side-chain prediction. *Journal of Computational Biology*, **2008**, 15, 899-911	1.7	30
29	FunHunt: model selection based on energy landscape characteristics. *Biochemical Society Transactions*, **2008**, 36, 1418-21	5.1	15
28	Discrimination of near-native structures in protein-protein docking by testing the stability of local minima. *Proteins: Structure, Function and Bioinformatics*, **2008**, 72, 993-1004	4.2	36
27	Trans protein splicing of cyanobacterial split inteins in endogenous and exogenous combinations. *Biochemistry*, **2007**, 46, 322-30	3.2	45
26	Minimizing and Learning Energy Functions for Side-Chain Prediction **2007**, 381-395		4
25	The structure, dynamics, and energetics of protein adsorption-lessons learned from adsorption of statherin to hydroxyapatite. *Magnetic Resonance in Chemistry*, **2007**, 45 Suppl 1, S32-47	2.1	41
24	RosettaDock in CAPRI rounds 6-12. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 758-63	4.2	26
23	Assessing the energy landscape of CAPRI targets by FunHunt. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 809-15	4.2	14
22	Learning MHC I--peptide binding. *Bioinformatics*, **2006**, 22, e227-35	7.2	74
21	Folding of the C-terminal bacterial binding domain in statherin upon adsorption onto hydroxyapatite crystals. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 16083-8	11.5	84
20	Is GAS1 a co-receptor for the GDNF family of ligands?. *Trends in Pharmacological Sciences*, **2006**, 27, 72-7	13.2	43
19	Identifying a common molecular mechanism for inhibition of MITF and STAT3 by PIAS3. *Blood*, **2006**, 107, 2839-45	2.2	24
18	Progress in modeling of protein structures and interactions. *Science*, **2005**, 310, 638-42	33.3	244
17	Improved side-chain modeling for protein-protein docking. *Protein Science*, **2005**, 14, 1328-39	6.3	182
16	Progress in protein-protein docking: atomic resolution predictions in the CAPRI experiment using RosettaDock with an improved treatment of side-chain flexibility. *Proteins: Structure, Function and Bioinformatics*, **2005**, 60, 187-94	4.2	87
15	A model of anthrax toxin lethal factor bound to protective antigen. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 16409-14	11.5	52
14	Conserved residue clustering and protein structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2003**, 52, 225-35	4.2	53
13	Protein-protein docking predictions for the CAPRI experiment. *Proteins: Structure, Function and Bioinformatics*, **2003**, 52, 118-22	4.2	93

12	Rosetta predictions in CASP5: successes, failures, and prospects for complete automation. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53 Suppl 6, 457-68	4.2	142
11	Protein-protein docking with simultaneous optimization of rigid-body displacement and side-chain conformations. *Journal of Molecular Biology*, **2003**, 331, 281-99	6.5	858
10	Examination of possible structural constraints of MHC-binding peptides by assessment of their native structure within their source proteins. *Proteins: Structure, Function and Bioinformatics*, **2001**, 45, 47-54	4.2	15
9	Structure-based prediction of binding peptides to MHC class I molecules: application to a broad range of MHC alleles. *Protein Science*, **2000**, 9, 1838-46	6.3	133
8	Knowledge-based structure prediction of MHC class I bound peptides: a study of 23 complexes. *Folding & Design*, **1998**, 3, 549-64		40
7	High-resolution global peptide-protein docking using fragments-based PIPER-FlexPepDock		2
6	Defining binding motifs and dynamics of the multi-pocket FERM domain from ezrin, radixin, moesin and merlin		1
5	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks		2
4	Structure-based prediction of KDAC6 substrates validated by enzymatic assay reveals determinants of promiscuity and detects new potential substrates		1
3	Harnessing protein folding neural networks for peptide-protein docking		2
2	Harnessing protein folding neural networks for peptide-protein docking		11
1	PatchMAN docking: Modeling peptide-protein interactions in the context of the receptor surface		1