

Dina Schneidman-Duhovny

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79
papers

8,265
citations

40
h-index

90
g-index

92
ext. papers

10,034
ext. citations

8.5
avg, IF

6.07
L-index

#	Paper	IF	Citations
79	PatchDock and SymmDock: servers for rigid and symmetric docking. <i>Nucleic Acids Research</i> , 2005 , 33, W363-7	20.1	1963
78	FireDock: a web server for fast interaction refinement in molecular docking. <i>Nucleic Acids Research</i> , 2008 , 36, W229-32	20.1	469
77	FoXS: a web server for rapid computation and fitting of SAXS profiles. <i>Nucleic Acids Research</i> , 2010 , 38, W540-4	20.1	403
76	UCSF Chimera, MODELLER, and IMP: an integrated modeling system. <i>Journal of Structural Biology</i> , 2012 , 179, 269-78	3.4	373
75	Putting the pieces together: integrative modeling platform software for structure determination of macromolecular assemblies. <i>PLoS Biology</i> , 2012 , 10, e1001244	9.7	362
74	Accurate SAXS profile computation and its assessment by contrast variation experiments. <i>Biophysical Journal</i> , 2013 , 105, 962-74	2.9	359
73	Mechanism of two classes of cancer mutations in the phosphoinositide 3-kinase catalytic subunit. <i>Science</i> , 2007 , 317, 239-42	33.3	314
72	FoXS, FoXSDock and MultiFoXS: Single-state and multi-state structural modeling of proteins and their complexes based on SAXS profiles. <i>Nucleic Acids Research</i> , 2016 , 44, W424-9	20.1	260
71	ModBase, a database of annotated comparative protein structure models, and associated resources. <i>Nucleic Acids Research</i> , 2011 , 39, D465-74	20.1	252
70	Taking geometry to its edge: fast unbound rigid (and hinge-bent) docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 107-12	4.2	217
69	ModBase, a database of annotated comparative protein structure models and associated resources. <i>Nucleic Acids Research</i> , 2014 , 42, D336-46	20.1	207
68	HingeProt: automated prediction of hinges in protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 1219-27	4.2	175
67	Geometry-based flexible and symmetric protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 224-31	4.2	155
66	PharmaGist: a webserver for ligand-based pharmacophore detection. <i>Nucleic Acids Research</i> , 2008 , 36, W223-8	20.1	150
65	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 710-728	5.5	145
64	Versatile and multivalent nanobodies efficiently neutralize SARS-CoV-2. <i>Science</i> , 2020 , 370, 1479-1484	33.3	138
63	Structural characterization by cross-linking reveals the detailed architecture of a coatomer-related heptameric module from the nuclear pore complex. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2927-43	7.6	122

62	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
61	CryptoSite: Expanding the Druggable Proteome by Characterization and Prediction of Cryptic Binding Sites. <i>Journal of Molecular Biology</i> , 2016 , 428, 709-719	6.5	110
60	An integrated suite of fast docking algorithms. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 3197-204	4.2	100
59	The SARS-CoV-2 Exerts a Distinctive Strategy for Interacting with the ACE2 Human Receptor. <i>Viruses</i> , 2020 , 12,	6.2	94
58	Recovering a representative conformational ensemble from underdetermined macromolecular structural data. <i>Journal of the American Chemical Society</i> , 2013 , 135, 16595-609	16.4	88
57	Optimized atomic statistical potentials: assessment of protein interfaces and loops. <i>Bioinformatics</i> , 2013 , 29, 3158-66	7.2	88
56	Macromolecular docking restrained by a small angle X-ray scattering profile. <i>Journal of Structural Biology</i> , 2011 , 173, 461-71	3.4	88
55	Novel approach for efficient pharmacophore-based virtual screening: method and applications. <i>Journal of Chemical Information and Modeling</i> , 2009 , 49, 2333-43	6.1	85
54	Integrative structural modeling with small angle X-ray scattering profiles. <i>BMC Structural Biology</i> , 2012 , 12, 17	2.7	80
53	A method for integrative structure determination of protein-protein complexes. <i>Bioinformatics</i> , 2012 , 28, 3282-9	7.2	69
52	Uncertainty in integrative structural modeling. <i>Current Opinion in Structural Biology</i> , 2014 , 28, 96-104	8.1	68
51	Predicting molecular interactions in silico: II. Protein-protein and protein-drug docking. <i>Current Medicinal Chemistry</i> , 2004 , 11, 91-107	4.3	68
50	The structural dynamics of macromolecular processes. <i>Current Opinion in Cell Biology</i> , 2009 , 21, 97-108	9	67
49	Statistical potential for modeling and ranking of protein-ligand interactions. <i>Journal of Chemical Information and Modeling</i> , 2011 , 51, 3078-92	6.1	61
48	CRB2 mutations produce a phenotype resembling congenital nephrosis, Finnish type, with cerebral ventriculomegaly and raised alpha-fetoprotein. <i>American Journal of Human Genetics</i> , 2015 , 96, 162-9	11	59
47	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
46	Integrative structure modeling of macromolecular assemblies from proteomics data. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1689-702	7.6	58
45	Formation of a repressive complex in the mammalian circadian clock is mediated by the secondary pocket of CRY1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 1560-1565	11.5	56

44	Identification of the N-terminal peptide binding site of glucose-regulated protein 94. <i>Journal of Biological Chemistry</i> , 2004 , 279, 16543-52	5.4	53
43	Deterministic pharmacophore detection via multiple flexible alignment of drug-like molecules. <i>Journal of Computational Biology</i> , 2008 , 15, 737-54	1.7	46
42	Automatic prediction of protein interactions with large scale motion. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 764-73	4.2	46
41	Cross-activating c-Met/ β integrin complex drives metastasis and invasive resistance in cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E8685-E8694	11.5	42
40	Assembly of macromolecular complexes by satisfaction of spatial restraints from electron microscopy images. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 18821-6	11.5	40
39	Molecular architecture of photoreceptor phosphodiesterase elucidated by chemical cross-linking and integrative modeling. <i>Journal of Molecular Biology</i> , 2014 , 426, 3713-3728	6.5	34
38	DksA regulates RNA polymerase in Escherichia coli through a network of interactions in the secondary channel that includes Sequence Insertion 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E6862-71	11.5	33
37	From structure to function: methods and applications. <i>Current Protein and Peptide Science</i> , 2005 , 6, 171-838		32
36	Integrative Structure Modeling: Overview and Assessment. <i>Annual Review of Biochemistry</i> , 2019 , 88, 113-135	29.1	29
35	Prion Protein-Antibody Complexes Characterized by Chromatography-Coupled Small-Angle X-Ray Scattering. <i>Biophysical Journal</i> , 2015 , 109, 793-805	2.9	28
34	Insights into HIV-1 proviral transcription from integrative structure and dynamics of the Tat:AFF4:P-TEFb:TAR complex. <i>ELife</i> , 2016 , 5,	8.9	28
33	Potent neutralizing nanobodies resist convergent circulating variants of SARS-CoV-2 by targeting diverse and conserved epitopes. <i>Nature Communications</i> , 2021 , 12, 4676	17.4	28
32	De novo, deleterious sequence variants that alter the transcriptional activity of the homeoprotein PBX1 are associated with intellectual disability and pleiotropic developmental defects. <i>Human Molecular Genetics</i> , 2017 , 26, 4849-4860	5.6	26
31	Expansion of phenotype and genotypic data in CRB2-related syndrome. <i>European Journal of Human Genetics</i> , 2016 , 24, 1436-44	5.3	26
30	Modeling of proteins and their assemblies with the Integrative Modeling Platform. <i>Methods in Molecular Biology</i> , 2014 , 1091, 277-95	1.4	25
29	Memdock: an α helical membrane protein docking algorithm. <i>Bioinformatics</i> , 2016 , 32, 2444-50	7.2	24
28	BioInfo3D: a suite of tools for structural bioinformatics. <i>Nucleic Acids Research</i> , 2004 , 32, W503-7	20.1	22
27	Modeling Structure and Dynamics of Protein Complexes with SAXS Profiles. <i>Methods in Molecular Biology</i> , 2018 , 1764, 449-473	1.4	19

26	Metabolic stereoselectivity of cytochrome P450 3A4 towards deoxypodophyllotoxin: In silico predictions and experimental validation. <i>European Journal of Medicinal Chemistry</i> , 2008 , 43, 1171-9	6.8	18
25	Approaching the CAPRI challenge with an efficient geometry-based docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 217-23	4.2	18
24	Predicting CD4 T-cell epitopes based on antigen cleavage, MHCII presentation, and TCR recognition. <i>PLoS ONE</i> , 2018 , 13, e0206654	3.7	17
23	Modeling of proteins and their assemblies with the integrative modeling platform. <i>Methods in Molecular Biology</i> , 2011 , 781, 377-97	1.4	16
22	Deterministic Pharmacophore Detection Via Multiple Flexible Alignment of Drug-Like Molecules. <i>Lecture Notes in Computer Science</i> , 2007 , 412-429	0.9	13
21	SAXS Merge: an automated statistical method to merge SAXS profiles using Gaussian processes. <i>Journal of Synchrotron Radiation</i> , 2014 , 21, 203-8	2.4	12
20	Integrative proteomics identifies thousands of distinct, multi-epitope, and high-affinity nanobodies. <i>Cell Systems</i> , 2021 , 12, 220-234.e9	10.6	12
19	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020 , 370,	33.3	11
18	Versatile, Multivalent Nanobody Cocktails Efficiently Neutralize SARS-CoV-2 2020 ,		10
17	Biallelic sequence variants in INTS1 in patients with developmental delays, cataracts, and craniofacial anomalies. <i>European Journal of Human Genetics</i> , 2019 , 27, 582-593	5.3	10
16	Targeted in situ cross-linking mass spectrometry and integrative modeling reveal the architectures of three proteins from SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	8
15	Modeling of Multimolecular Complexes. <i>Methods in Molecular Biology</i> , 2020 , 2112, 163-174	1.4	8
14	Biallelic variants in the RNA exosome gene EXOSC5 are associated with developmental delays, short stature, cerebellar hypoplasia and motor weakness. <i>Human Molecular Genetics</i> , 2020 , 29, 2218-2239	5.6	7
13	Potent neutralizing nanobodies resist convergent circulating variants of SARS-CoV-2 by targeting novel and conserved epitopes 2021 ,		7
12	Cryo-EM structures of engineered active bc-cbb type CIICIV super-complexes and electronic communication between the complexes. <i>Nature Communications</i> , 2021 , 12, 929	17.4	7
11	Reconstruction of 3D structures of MET antibodies from electron microscopy 2D class averages. <i>PLoS ONE</i> , 2017 , 12, e0175758	3.7	6
10	Structural Characterization of Full-Length Human Dehydrodolichyl Diphosphate Synthase Using an Integrative Computational and Experimental Approach. <i>Biomolecules</i> , 2019 , 9,	5.9	5
9	Probing Oligomerized Conformations of Defensin in the Membrane. <i>Methods in Molecular Biology</i> , 2017 , 1529, 353-362	1.4	4

8	Dynamic Evolution of the Cthrc1 Genes, a Newly Defined Collagen-Like Family. <i>Genome Biology and Evolution</i> , 2020 , 12, 3957-3970	3.9	4
7	A robust and versatile nanobody platform for drug delivery		4
6	A resource of high-quality and versatile nanobodies for drug delivery. <i>iScience</i> , 2021 , 24, 103014	6.1	4
5	Structural similarity of genetically interacting proteins. <i>BMC Systems Biology</i> , 2008 , 2, 69	3.5	3
4	Integrative proteomics reveals exceptional diversity and versatility of mammalian humoral immunity		3
3	De novo STXBP1 mutation in a child with developmental delay and spasticity reveals a major structural alteration in the interface with syntaxin 1A. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020 , 183, 412-422	3.5	2
2	NanoNet: Rapid end-to-end nanobody modeling by deep learning at sub angstrom resolution		1
1	Integrative structure determination reveals functional global flexibility for an ultra-multimodular arabinanase.. <i>Communications Biology</i> , 2022 , 5, 465	6.7	1