Dina Schneidman-Duhovny

List of Publications by Year in Descending Order

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	Integrative structure determination reveals functional global flexibility for an ultra-multimodular arabinanase.. *Communications Biology*, **2022**, 5, 465	6.7	1
78	Potent neutralizing nanobodies resist convergent circulating variants of SARS-CoV-2 by targeting novel and conserved epitopes **2021**,		7
77	Integrative proteomics identifies thousands of distinct, multi-epitope, and high-affinity nanobodies. *Cell Systems*, **2021**, 12, 220-234.e9	10.6	12
76	Cryo-EM structures of engineered active bc-cbb type CIIICIV super-complexes and electronic communication between the complexes. *Nature Communications*, **2021**, 12, 929	17.4	7
75	Targeted in situ cross-linking mass spectrometry and integrative modeling reveal the architectures of three proteins from SARS-CoV-2. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	8
74	Potent neutralizing nanobodies resist convergent circulating variants of SARS-CoV-2 by targeting diverse and conserved epitopes. *Nature Communications*, **2021**, 12, 4676	17.4	28
73	A resource of high-quality and versatile nanobodies for drug delivery. *IScience*, **2021**, 24, 103014	6.1	4
72	Genetic interaction mapping informs integrative structure determination of protein complexes. *Science*, **2020**, 370,	33.3	11
71	Versatile and multivalent nanobodies efficiently neutralize SARS-CoV-2. *Science*, **2020**, 370, 1479-1484	33.3	138
70	The SARS-CoV-2 Exerts a Distinctive Strategy for Interacting with the ACE2 Human Receptor. *Viruses*, **2020**, 12,	6.2	94
69	Biallelic variants in the RNA exosome gene EXOSC5 are associated with developmental delays, short stature, cerebellar hypoplasia and motor weakness. *Human Molecular Genetics*, **2020**, 29, 2218-2229	5.6	7
68	Dynamic Evolution of the Cthrc1 Genes, a Newly Defined Collagen-Like Family. *Genome Biology and Evolution*, **2020**, 12, 3957-3970	3.9	4
67	Versatile, Multivalent Nanobody Cocktails Efficiently Neutralize SARS-CoV-2 **2020**,		10
66	De novo STXBP1 mutation in a child with developmental delay and spasticity reveals a major structural alteration in the interface with syntaxin 1A. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2020**, 183, 412-422	3.5	2
65	Modeling of Multimolecular Complexes. *Methods in Molecular Biology*, **2020**, 2112, 163-174	1.4	8
64	Integrative Structure Modeling: Overview and Assessment. *Annual Review of Biochemistry*, **2019**, 88, 113-135	29.1	29
63	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1200-1221	4.2	58

62	Structural Characterization of Full-Length Human Dehydrodolichyl Diphosphate Synthase Using an Integrative Computational and Experimental Approach. *Biomolecules*, **2019**, 9,	5.9	5
61	Biallelic sequence variants in INTS1 in patients with developmental delays, cataracts, and craniofacial anomalies. *European Journal of Human Genetics*, **2019**, 27, 582-593	5.3	10
60	Modeling Structure and Dynamics of Protein Complexes with SAXS Profiles. *Methods in Molecular Biology*, **2018**, 1764, 449-473	1.4	19
59	Predicting CD4 T-cell epitopes based on antigen cleavage, MHCII presentation, and TCR recognition. *PLoS ONE*, **2018**, 13, e0206654	3.7	17
58	Formation of a repressive complex in the mammalian circadian clock is mediated by the secondary pocket of CRY1. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 1560-1565	11.5	56
57	Probing Oligomerized Conformations of Defensin in the Membrane. *Methods in Molecular Biology*, **2017**, 1529, 353-362	1.4	4
56	Cross-activating c-Met/β1 integrin complex drives metastasis and invasive resistance in cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E8685-E8694	11.5	42
55	De novo, deleterious sequence variants that alter the transcriptional activity of the homeoprotein PBX1 are associated with intellectual disability and pleiotropic developmental defects. *Human Molecular Genetics*, **2017**, 26, 4849-4860	5.6	26
54	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. *Acta Crystallographica Section D: Structural Biology*, **2017**, 73, 710-728	5.5	145
53	Reconstruction of 3D structures of MET antibodies from electron microscopy 2D class averages. *PLoS ONE*, **2017**, 12, e0175758	3.7	6
52	Expansion of phenotype and genotypic data in CRB2-related syndrome. *European Journal of Human Genetics*, **2016**, 24, 1436-44	5.3	26
51	CryptoSite: Expanding the Druggable Proteome by Characterization and Prediction of Cryptic Binding Sites. *Journal of Molecular Biology*, **2016**, 428, 709-719	6.5	110
50	Insights into HIV-1 proviral transcription from integrative structure and dynamics of the Tat:AFF4:P-TEFb:TAR complex. *ELife*, **2016**, 5,	8.9	28
49	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 323-48	4.2	111
48	FoXS, FoXSDock and MultiFoXS: Single-state and multi-state structural modeling of proteins and their complexes based on SAXS profiles. *Nucleic Acids Research*, **2016**, 44, W424-9	20.1	260
47	Memdock: an α-helical membrane protein docking algorithm. *Bioinformatics*, **2016**, 32, 2444-50	7.2	24
46	Prion Protein-Antibody Complexes Characterized by Chromatography-Coupled Small-Angle X-Ray Scattering. *Biophysical Journal*, **2015**, 109, 793-805	2.9	28
45	DksA regulates RNA polymerase in Escherichia coli through a network of interactions in the secondary channel that includes Sequence Insertion 1. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E6862-71	11.5	33

44	CRB2 mutations produce a phenotype resembling congenital nephrosis, Finnish type, with cerebral ventriculomegaly and raised alpha-fetoprotein. *American Journal of Human Genetics*, **2015**, 96, 162-9	11	59
43	Modeling of proteins and their assemblies with the Integrative Modeling Platform. *Methods in Molecular Biology*, **2014**, 1091, 277-95	1.4	25
42	Uncertainty in integrative structural modeling. *Current Opinion in Structural Biology*, **2014**, 28, 96-104	8.1	68
41	Molecular architecture of photoreceptor phosphodiesterase elucidated by chemical cross-linking and integrative modeling. *Journal of Molecular Biology*, **2014**, 426, 3713-3728	6.5	34
40	Structural characterization by cross-linking reveals the detailed architecture of a coatomer-related heptameric module from the nuclear pore complex. *Molecular and Cellular Proteomics*, **2014**, 13, 2927-43	7.6	122
39	ModBase, a database of annotated comparative protein structure models and associated resources. *Nucleic Acids Research*, **2014**, 42, D336-46	20.1	207
38	SAXS Merge: an automated statistical method to merge SAXS profiles using Gaussian processes. *Journal of Synchrotron Radiation*, **2014**, 21, 203-8	2.4	12
37	Accurate SAXS profile computation and its assessment by contrast variation experiments. *Biophysical Journal*, **2013**, 105, 962-74	2.9	359
36	Recovering a representative conformational ensemble from underdetermined macromolecular structural data. *Journal of the American Chemical Society*, **2013**, 135, 16595-609	16.4	88
35	Optimized atomic statistical potentials: assessment of protein interfaces and loops. *Bioinformatics*, **2013**, 29, 3158-66	7.2	88
34	UCSF Chimera, MODELLER, and IMP: an integrated modeling system. *Journal of Structural Biology*, **2012**, 179, 269-78	3.4	373
33	Integrative structural modeling with small angle X-ray scattering profiles. *BMC Structural Biology*, **2012**, 12, 17	2.7	80
32	Putting the pieces together: integrative modeling platform software for structure determination of macromolecular assemblies. *PLoS Biology*, **2012**, 10, e1001244	9.7	362
31	Assembly of macromolecular complexes by satisfaction of spatial restraints from electron microscopy images. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 18821-6	11.5	40
30	A method for integrative structure determination of protein-protein complexes. *Bioinformatics*, **2012**, 28, 3282-9	7.2	69
29	Macromolecular docking restrained by a small angle X-ray scattering profile. *Journal of Structural Biology*, **2011**, 173, 461-71	3.4	88
28	Statistical potential for modeling and ranking of protein-ligand interactions. *Journal of Chemical Information and Modeling*, **2011**, 51, 3078-92	6.1	61
27	ModBase, a database of annotated comparative protein structure models, and associated resources. *Nucleic Acids Research*, **2011**, 39, D465-74	20.1	252

26	Modeling of proteins and their assemblies with the integrative modeling platform. *Methods in Molecular Biology*, **2011**, 781, 377-97	1.4	16
25	FoXS: a web server for rapid computation and fitting of SAXS profiles. *Nucleic Acids Research*, **2010**, 38, W540-4	20.1	403
24	Integrative structure modeling of macromolecular assemblies from proteomics data. *Molecular and Cellular Proteomics*, **2010**, 9, 1689-702	7.6	58
23	An integrated suite of fast docking algorithms. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 3197-204	4.2	100
22	The structural dynamics of macromolecular processes. *Current Opinion in Cell Biology*, **2009**, 21, 97-108	9	67
21	Novel approach for efficient pharmacophore-based virtual screening: method and applications. *Journal of Chemical Information and Modeling*, **2009**, 49, 2333-43	6.1	85
20	Structural similarity of genetically interacting proteins. *BMC Systems Biology*, **2008**, 2, 69	3.5	3
19	Deterministic pharmacophore detection via multiple flexible alignment of drug-like molecules. *Journal of Computational Biology*, **2008**, 15, 737-54	1.7	46
18	FireDock: a web server for fast interaction refinement in molecular docking. *Nucleic Acids Research*, **2008**, 36, W229-32	20.1	469
17	PharmaGist: a webserver for ligand-based pharmacophore detection. *Nucleic Acids Research*, **2008**, 36, W223-8	20.1	150
16	HingeProt: automated prediction of hinges in protein structures. *Proteins: Structure, Function and Bioinformatics*, **2008**, 70, 1219-27	4.2	175
15	Metabolic stereoselectivity of cytochrome P450 3A4 towards deoxypodophyllotoxin: In silico predictions and experimental validation. *European Journal of Medicinal Chemistry*, **2008**, 43, 1171-9	6.8	18
14	Automatic prediction of protein interactions with large scale motion. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 764-73	4.2	46
13	Mechanism of two classes of cancer mutations in the phosphoinositide 3-kinase catalytic subunit. *Science*, **2007**, 317, 239-42	33.3	314
12	Deterministic Pharmacophore Detection Via Multiple Flexible Alignment of Drug-Like Molecules. *Lecture Notes in Computer Science*, **2007**, 412-429	0.9	13
11	PatchDock and SymmDock: servers for rigid and symmetric docking. *Nucleic Acids Research*, **2005**, 33, W363-7	20.1	1963
10	Approaching the CAPRI challenge with an efficient geometry-based docking. *Proteins: Structure, Function and Bioinformatics*, **2005**, 60, 217-23	4.2	18
9	Geometry-based flexible and symmetric protein docking. *Proteins: Structure, Function and Bioinformatics*, **2005**, 60, 224-31	4.2	155

8	From structure to function: methods and applications. *Current Protein and Peptide Science*, **2005**, 6, 171-83	2.8	32
7	Predicting molecular interactions in silico: II. Protein-protein and protein-drug docking. *Current Medicinal Chemistry*, **2004**, 11, 91-107	4.3	68
6	BioInfo3D: a suite of tools for structural bioinformatics. *Nucleic Acids Research*, **2004**, 32, W503-7	20.1	22
5	Identification of the N-terminal peptide binding site of glucose-regulated protein 94. *Journal of Biological Chemistry*, **2004**, 279, 16543-52	5.4	53
4	Taking geometry to its edge: fast unbound rigid (and hinge-bent) docking. *Proteins: Structure, Function and Bioinformatics*, **2003**, 52, 107-12	4.2	217
3	A robust and versatile nanobody platform for drug delivery		4
2	Integrative proteomics reveals exceptional diversity and versatility of mammalian humoral immunity		3
1	NanoNet: Rapid end-to-end nanobody modeling by deep learning at sub angstrom resolution		1