Sarel J Fleishman

List of Publications by Year in Descending Order

88 papers	5,713 citations	36 h-index	75 g-index
110 ext. papers	7,041 ext. citations	9.9 avg, IF	5.61 L-index

#	Paper	IF	Citations
88	Computationally designed dual-color MRI reporters for noninvasive imaging of transgene expression.. *Nature Biotechnology*, **2022**,	44.5	4
87	Computer-aided engineering of staphylokinase toward enhanced affinity and selectivity for plasmin.. *Computational and Structural Biotechnology Journal*, **2022**, 20, 1366-1377	6.8	0
86	Stable and Functionally Diverse Versatile Peroxidases Designed Directly from Sequences.. *Journal of the American Chemical Society*, **2022**, 144, 3564-3571	16.4	4
85	What Have We Learned from Design of Function in Large Proteins?. *Biodesign Research*, **2022**, 2022, 1-11	3.1	2
84	A Rationally and Computationally Designed Fluorescent Biosensor for d-Serine. *ACS Sensors*, **2021**, 6, 4193-4205	9.2	1
83	Computationally designed pyocyanin demethylase acts synergistically with tobramycin to kill recalcitrant biofilms. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	10
82	Extending the New Generation of Structure Predictors to Account for Dynamics and Allostery. *Journal of Molecular Biology*, **2021**, 433, 167007	6.5	6
81	Community-Wide Experimental Evaluation of the PROSS Stability-Design Method. *Journal of Molecular Biology*, **2021**, 433, 166964	6.5	8
80	Computational Enzyme Engineering Pipelines for Optimized Production of Renewable Chemicals. *Frontiers in Bioengineering and Biotechnology*, **2021**, 9, 673005	5.8	1
79	Local Mutations Can Serve as a Game Changer for Global Protein Solvent Interaction. *Jacs Au*, **2021**, 1, 1076-1085		5
78	The AbDesign computational pipeline for modular backbone assembly and design of binders and enzymes. *Protein Science*, **2021**, 30, 151-159	6.3	7
77	Biomolecular Recognition of the Glycan Neoantigen CA19-9 by Distinct Antibodies. *Journal of Molecular Biology*, **2021**, 433, 167099	6.5	1
76	Direct-MS analysis of antibody-antigen complexes. *Proteomics*, **2021**, 21, e2000300	4.8	1
75	The neutralization potency of anti-SARS-CoV-2 therapeutic human monoclonal antibodies is retained against viral variants. *Cell Reports*, **2021**, 36, 109679	10.6	3
74	Practically useful protein-design methods combining phylogenetic and atomistic calculations. *Current Opinion in Structural Biology*, **2020**, 63, 58-64	8.1	16
73	One-step sequence and structure-guided optimization of HIV-1 envelope gp140. *Current Research in Structural Biology*, **2020**, 2, 45-55	2.8	6
72	PROSS 2: a new server for the design of stable and highly expressed protein variants. *Bioinformatics* , **2020**,	7.2	5

71	Design of a basigin-mimicking inhibitor targeting the malaria invasion protein RH5. *Proteins: Structure, Function and Bioinformatics*, **2020**, 88, 187-195	4.2	3
70	A lipophilicity-based energy function for membrane-protein modelling and design. *PLoS Computational Biology*, **2019**, 15, e1007318	5	16
69	Optimizing antibody affinity and stability by the automated design of the variable light-heavy chain interfaces. *PLoS Computational Biology*, **2019**, 15, e1007207	5	31
68	AbPredict 2: a server for accurate and unstrained structure prediction of antibody variable domains. *Bioinformatics*, **2019**, 35, 1591-1593	7.2	10
67	Principles of Protein Stability and Their Application in Computational Design. *Annual Review of Biochemistry*, **2018**, 87, 105-129	29.1	106
66	Highly active enzymes by automated combinatorial backbone assembly and sequence design. *Nature Communications*, **2018**, 9, 2780	17.4	32
65	A combined computational-experimental approach to define the structural origin of antibody recognition of sialyl-Tn, a tumor-associated carbohydrate antigen. *Scientific Reports*, **2018**, 8, 10786	4.9	11
64	Estimating Interprotein Pairwise Interaction Energies in Cell Lysates from a Single Native Mass Spectrum. *Analytical Chemistry*, **2018**, 90, 10090-10094	7.8	12
63	Manipulating the Folding Landscape of a Multidomain Protein. *Journal of Physical Chemistry B*, **2018**, 122, 11030-11038	3.4	12
62	Design and in vitro realization of carbon-conserving photorespiration. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E11455-E11464	11.5	66
61	Ultrahigh specificity in a network of computationally designed protein-interaction pairs. *Nature Communications*, **2018**, 9, 5286	17.4	32
60	Automated Design of Efficient and Functionally Diverse Enzyme Repertoires. *Molecular Cell*, **2018**, 72, 178-186.e5	17.6	79
59	One-step design of a stable variant of the malaria invasion protein RH5 for use as a vaccine immunogen. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 998-1002	11.5	44
58	Incorporating an allosteric regulatory site in an antibody through backbone design. *Protein Science*, **2017**, 26, 807-813	6.3	9
57	Overcoming an optimization plateau in the directed evolution of highly efficient nerve agent bioscavengers. *Protein Engineering, Design and Selection*, **2017**, 30, 333-345	1.9	41
56	Collective repacking reveals that the structures of protein cores are uniquely specified by steric repulsive interactions. *Protein Engineering, Design and Selection*, **2017**, 30, 387-394	1.9	6
55	Local energetic frustration affects the dependence of green fluorescent protein folding on the chaperonin GroEL. *Journal of Biological Chemistry*, **2017**, 292, 20583-20591	5.4	19
54	Principles for computational design of binding antibodies. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 10900-10905	11.5	73

53	Improved antibody-based ricin neutralization by affinity maturation is correlated with slower off-rate values. *Protein Engineering, Design and Selection*, **2017**, 30, 611-617	1.9	13
52	High-accuracy modeling of antibody structures by a search for minimum-energy recombination of backbone fragments. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 30-38	4.2	14
51	Interplay between hydrophobicity and the positive-inside rule in determining membrane-protein topology. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 10340-5	11.5	26
50	Automated Structure- and Sequence-Based Design of Proteins for High Bacterial Expression and Stability. *Molecular Cell*, **2016**, 63, 337-346	17.6	204
49	Why reinvent the wheel? Building new proteins based on ready-made parts. *Protein Science*, **2016**, 25, 1179-87	6.3	28
48	Overcoming a species-specificity barrier in development of an inhibitory antibody targeting a modulator of tumor stroma. *Protein Engineering, Design and Selection*, **2016**, 29, 135-47	1.9	7
47	Mutational scanning reveals the determinants of protein insertion and association energetics in the plasma membrane. *ELife*, **2016**, 5,	8.9	43
46	PROTEIN DESIGN. Inspired by nature. *Science*, **2016**, 352, 657-8	33.3	8
45	Computationally Designed Armadillo Repeat Proteins for Modular Peptide Recognition. *Journal of Molecular Biology*, **2016**, 428, 4467-4489	6.5	12
44	Dominant Mutations in the Autoimmune Regulator AIRE Are Associated with Common Organ-Specific Autoimmune Diseases. *Immunity*, **2015**, 42, 1185-96	32.3	156
43	Combined Crystal Structure of a Type I Cohesin: MUTATION AND AFFINITY BINDING STUDIES REVEAL STRUCTURAL DETERMINANTS OF COHESIN-DOCKERIN SPECIFICITIES. *Journal of Biological Chemistry*, **2015**, 290, 16215-25	5.4	9
42	AbDesign: An algorithm for combinatorial backbone design guided by natural conformations and sequences. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 1385-406	4.2	55
41	Computational design of a pH-sensitive IgG binding protein. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 675-80	11.5	57
40	A "fuzzy"-logic language for encoding multiple physical traits in biomolecules. *Journal of Molecular Biology*, **2014**, 426, 4125-4138	6.5	16
39	Computational design of protein-protein interactions. *Current Opinion in Structural Biology*, **2013**, 23, 903-10	8.1	46
38	Computational design of a protein-based enzyme inhibitor. *Journal of Molecular Biology*, **2013**, 425, 3563-75	4.75	71
37	Emerging themes in the computational design of novel enzymes and protein-protein interfaces. *FEBS Letters*, **2013**, 587, 1147-54	3.8	41
36	Computational protein design suggests that human PCNA-partner interactions are not optimized for affinity. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 341-8	4.2	8

35	Computational design of novel protein binders and experimental affinity maturation. *Methods in Enzymology*, **2013**, 523, 1-19	1.7	30
34	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 1980-7	4.2	78
33	Structure of the ultra-high-affinity colicin E2 DNase--Im2 complex. *Journal of Molecular Biology*, **2012**, 417, 79-94	6.5	45
32	Role of the biomolecular energy gap in protein design, structure, and evolution. *Cell*, **2012**, 149, 262-73	56.2	83
31	Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing. *Nature Biotechnology*, **2012**, 30, 543-8	44.5	279
30	ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules. *Methods in Enzymology*, **2011**, 487, 545-74	1.7	1216
29	Hotspot-centric de novo design of protein binders. *Journal of Molecular Biology*, **2011**, 413, 1047-62	6.5	32
28	Community-wide assessment of protein-interface modeling suggests improvements to design methodology. *Journal of Molecular Biology*, **2011**, 414, 289-302	6.5	114
27	RosettaScripts: a scripting language interface to the Rosetta macromolecular modeling suite. *PLoS ONE*, **2011**, 6, e20161	3.7	311
26	Computational design of proteins targeting the conserved stem region of influenza hemagglutinin. *Science*, **2011**, 332, 816-21	33.3	441
25	Restricted sidechain plasticity in the structures of native proteins and complexes. *Protein Science*, **2011**, 20, 753-7	6.3	37
24	High-resolution mapping of protein sequence-function relationships. *Nature Methods*, **2010**, 7, 741-6	21.6	350
23	The structural and energetic basis for high selectivity in a high-affinity protein-protein interaction. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 10080-5	11.5	101
22	Rosetta in CAPRI rounds 13-19. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 3212-8	4.2	17
21	A new twist in TCR diversity revealed by a forbidden alphabeta TCR. *Journal of Molecular Biology*, **2008**, 375, 1306-19	6.5	21
20	RosettaDock in CAPRI rounds 6-12. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 758-63	4.2	26
19	Prediction and simulation of motion in pairs of transmembrane alpha-helices. *Bioinformatics*, **2007**, 23, e212-8	7.2	17
18	Co-evolving residues in membrane proteins. *Bioinformatics*, **2007**, 23, 3312-9	7.2	57

17	Progress in structure prediction of alpha-helical membrane proteins. *Current Opinion in Structural Biology*, **2006**, 16, 496-504	8.1	55
16	Transmembrane protein structures without X-rays. *Trends in Biochemical Sciences*, **2006**, 31, 106-13	10.3	71
15	Has the code for protein translocation been broken?. *Trends in Biochemical Sciences*, **2006**, 31, 192-6	10.3	17
14	Intrinsically disordered C-terminal segments of voltage-activated potassium channels: a possible fishing rod-like mechanism for channel binding to scaffold proteins. *Bioinformatics*, **2006**, 22, 1546-50	7.2	32
13	The structural context of disease-causing mutations in gap junctions. *Journal of Biological Chemistry* , **2006**, 281, 28958-63	5.4	12
12	Quasi-symmetry in the cryo-EM structure of EmrE provides the key to modeling its transmembrane domain. *Journal of Molecular Biology*, **2006**, 364, 54-67	6.5	102
11	Assigning transmembrane segments to helices in intermediate-resolution structures. *Bioinformatics* , **2004**, 20 Suppl 1, i122-9	7.2	13
10	A putative mechanism for downregulation of the catalytic activity of the EGF receptor via direct contact between its kinase and C-terminal domains. *Structure*, **2004**, 12, 2265-75	5.2	57
9	Free diffusion of steroid hormones across biomembranes: a simplex search with implicit solvent model calculations. *Biophysical Journal*, **2004**, 87, 768-79	2.9	81
8	An automatic method for predicting transmembrane protein structures using cryo-EM and evolutionary data. *Biophysical Journal*, **2004**, 87, 3448-59	2.9	48
7	A Calpha model for the transmembrane alpha helices of gap junction intercellular channels. *Molecular Cell*, **2004**, 15, 879-88	17.6	100
6	An evolutionarily conserved network of amino acids mediates gating in voltage-dependent potassium channels. *Journal of Molecular Biology*, **2004**, 340, 307-18	6.5	52
5	pANT: a method for the pairwise assessment of nonfunctionalization times of processed pseudogenes. *Molecular Biology and Evolution*, **2003**, 20, 1876-80	8.3	8
4	A putative molecular-activation switch in the transmembrane domain of erbB2. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 15937-40	11.5	220
3	A novel scoring function for predicting the conformations of tightly packed pairs of transmembrane alpha-helices. *Journal of Molecular Biology*, **2002**, 321, 363-78	6.5	68
2	De novodesigned receptor transmembrane domains enhance CAR-T cell cytotoxicity and attenuate cytokine release		1
1	A computationally designed fluorescent biosensor for D-serine		3