Sarel J Fleishman

List of Publications by Year
in descending order

92	7,936	81900 39	56724 83
papers	citations	h-index	g-index

110	110	110	9385
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Rosetta3. Methods in Enzymology, 2011, 487, 545-574.	1.0	1,620
2	Computational Design of Proteins Targeting the Conserved Stem Region of Influenza Hemagglutinin. Science, 2011, 332, 816-821.	12.6	527
3	RosettaScripts: A Scripting Language Interface to the Rosetta Macromolecular Modeling Suite. PLoS ONE, 2011, 6, e20161.	2.5	506
4	High-resolution mapping of protein sequence-function relationships. Nature Methods, 2010, 7, 741-746.	19.0	482
5	Automated Structure- and Sequence-Based Design of Proteins for High Bacterial Expression and Stability. Molecular Cell, 2016, 63, 337-346.	9.7	363
6	Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing. Nature Biotechnology, 2012, 30, 543-548.	17.5	342
7	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, 15937-15940.	7.1	247
8	Dominant Mutations in the Autoimmune Regulator AIRE Are Associated with Common Organ-Specific Autoimmune Diseases. Immunity, 2015, 42, 1185-1196.	14.3	246
9	Principles of Protein Stability and Their Application in Computational Design. Annual Review of Biochemistry, 2018, 87, 105-129.	11.1	187
10	Automated Design of Efficient and Functionally Diverse Enzyme Repertoires. Molecular Cell, 2018, 72, 178-186.e5.	9.7	165
11	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
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.	4.2	114
13	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, 10080-10085.	7.1	112
14	A CÎ± Model for the Transmembrane Î± Helices of Gap Junction Intercellular Channels. Molecular Cell, 2004, 15, 879-888.	9.7	107
15	Principles for computational design of binding antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10900-10905.	7.1	106
16	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.	7.1	97
17	Role of the Biomolecular Energy Gap in Protein Design, Structure, and Evolution. Cell, 2012, 149, 262-273.	28.9	94
18	Free Diffusion of Steroid Hormones Across Biomembranes: A Simplex Search with Implicit Solvent Model Calculations. Biophysical Journal, 2004, 87, 768-779.	0.5	93

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19	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	2.6	87
20	AbDesign: An algorithm for combinatorial backbone design guided by natural conformations and sequences. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1385-1406.	2.6	86
21	Computational Design of a Protein-Based Enzyme Inhibitor. Journal of Molecular Biology, 2013, 425, 3563-3575.	4.2	85
22	Transmembrane protein structures without X-rays. Trends in Biochemical Sciences, 2006, 31, 106-113.	7.5	84
23	Optimizing antibody affinity and stability by the automated design of the variable light-heavy chain interfaces. PLoS Computational Biology, 2019, 15, e1007207.	3.2	77
24	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.	7.1	75
25	A Novel Scoring Function for Predicting the Conformations of Tightly Packed Pairs of Transmembrane Î±-Helices. Journal of Molecular Biology, 2002, 321, 363-378.	4.2	74
26	Computational design of a pH-sensitive IgG binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 675-680.	7.1	74
27	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, 2265-2275.	3.3	66
28	Mutational scanning reveals the determinants of protein insertion and association energetics in the plasma membrane. ELife, 2016, 5, .	6.0	66
29	Co-evolving residues in membrane proteins. Bioinformatics, 2007, 23, 3312-3319.	4.1	65
30	Progress in structure prediction of Î±-helical membrane proteins. Current Opinion in Structural Biology, 2006, 16, 496-504.	5.7	61
31	An Evolutionarily Conserved Network of Amino Acids Mediates Gating in Voltage-dependent Potassium Channels. Journal of Molecular Biology, 2004, 340, 307-318.	4.2	59
32	Overcoming an optimization plateau in the directed evolution of highly efficient nerve agent bioscavengers. Protein Engineering, Design and Selection, 2017, 30, 333-345.	2.1	57
33	Structure of the Ultra-High-Affinity Colicin E2 DNaseâ€“Im2 Complex. Journal of Molecular Biology, 2012, 417, 79-94.	4.2	54
34	Computational design of proteinâ€“protein interactions. Current Opinion in Structural Biology, 2013, 23, 903-910.	5.7	53
35	An Automatic Method for Predicting Transmembrane Protein Structures Using Cryo-EM and Evolutionary Data. Biophysical Journal, 2004, 87, 3448-3459.	0.5	51
36	Restricted sidechain plasticity in the structures of native proteins and complexes. Protein Science, 2011, 20, 753-757.	7.6	50

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37	Ultrahigh specificity in a network of computationally designed protein-interaction pairs. Nature Communications, 2018, 9, 5286.	12.8	49
38	Emerging themes in the computational design of novel enzymes and proteinâ€“protein interfaces. FEBS Letters, 2013, 587, 1147-1154.	2.8	46
39	Highly active enzymes by automated combinatorial backbone assembly and sequence design. Nature Communications, 2018, 9, 2780.	12.8	45
40	Community-Wide Experimental Evaluation of the PROSS Stability-Design Method. Journal of Molecular Biology, 2021, 433, 166964.	4.2	42
41	Hotspot-Centric De Novo Design of Protein Binders. Journal of Molecular Biology, 2011, 413, 1047-1062.	4.2	41
42	Computational Design of Novel Protein Binders and Experimental Affinity Maturation. Methods in Enzymology, 2013, 523, 1-19.	1.0	38
43	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, 10340-10345.	7.1	38
44	Structure and receptor recognition by the Lassa virus spike complex. Nature, 2022, 603, 174-179.	27.8	37
45	Practically useful protein-design methods combining phylogenetic and atomistic calculations. Current Opinion in Structural Biology, 2020, 63, 58-64.	5.7	36
46	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, 1546-1550.	4.1	35
47	PROSS 2: a new server for the design of stable and highly expressed protein variants. Bioinformatics, 2021, 37, 123-125.	4.1	35
48	Why reinvent the wheel? Building new proteins based on readyâ€made parts. Protein Science, 2016, 25, 1179-1187.	7.6	33
49	A lipophilicity-based energy function for membrane-protein modelling and design. PLoS Computational Biology, 2019, 15, e1007318.	3.2	32
50	Computationally designed pyocyanin demethylase acts synergistically with tobramycin to kill recalcitrant Pseudomonas aeruginosa biofilms. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	31
51	Stable and Functionally Diverse Versatile Peroxidases Designed Directly from Sequences. Journal of the American Chemical Society, 2022, 144, 3564-3571.	13.7	30
52	RosettaDock in CAPRI rounds 6â€“12. Proteins: Structure, Function and Bioinformatics, 2007, 69, 758-763.	2.6	26
53	Local energetic frustration affects the dependence of green fluorescent protein folding on the chaperonin GroEL. Journal of Biological Chemistry, 2017, 292, 20583-20591.	3.4	26
54	A â€œFuzzyâ€•Logic Language for Encoding Multiple Physical Traits in Biomolecules. Journal of Molecular Biology, 2014, 426, 4125-4138.	4.2	25

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55	Manipulating the Folding Landscape of a Multidomain Protein. Journal of Physical Chemistry B, 2018, 122, 11030-11038.	2.6	24
56	Highâ€accuracy modeling of antibody structures by a search for minimumâ€energy recombination of backbone fragments. Proteins: Structure, Function and Bioinformatics, 2017, 85, 30-38.	2.6	23
57	A New Twist in TCR Diversity Revealed by a Forbidden Î±Î² TCR. Journal of Molecular Biology, 2008, 375, 1306-1319.	4.2	21
58	Rosetta in CAPRI rounds 13â€“19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3212-3218.	2.6	20
59	Extending the New Generation of Structure Predictors to Account for Dynamics and Allostery. Journal of Molecular Biology, 2021, 433, 167007.	4.2	20
60	Computationally Designed Armadillo Repeat Proteins for Modular Peptide Recognition. Journal of Molecular Biology, 2016, 428, 4467-4489.	4.2	19
61	De novo-designed transmembrane domains tune engineered receptor functions. ELife, 2022, 11, .	6.0	19
62	Has the code for protein translocation been broken?. Trends in Biochemical Sciences, 2006, 31, 192-196.	7.5	18
63	Prediction and simulation of motion in pairs of transmembrane Â-helices. Bioinformatics, 2007, 23, e212-e218.	4.1	18
64	AbPredict 2: a server for accurate and unstrained structure prediction of antibody variable domains. Bioinformatics, 2019, 35, 1591-1593.	4.1	18
65	Computationally designed dual-color MRI reporters for noninvasive imaging of transgene expression. Nature Biotechnology, 2022, 40, 1143-1149.	17.5	18
66	Estimating Interprotein Pairwise Interaction Energies in Cell Lysates from a Single Native Mass Spectrum. Analytical Chemistry, 2018, 90, 10090-10094.	6.5	17
67	Improved antibody-based ricin neutralization by affinity maturation is correlated with slower off-rate values. Protein Engineering, Design and Selection, 2017, 30, 611-617.	2.1	15
68	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.	3.3	15
69	The <scp>AbDesign</scp> computational pipeline for modular backbone assembly and design of binders and enzymes. Protein Science, 2021, 30, 151-159.	7.6	15
70	The Structural Context of Disease-causing Mutations in Gap Junctions. Journal of Biological Chemistry, 2006, 281, 28958-28963.	3.4	14
71	Computational Enzyme Engineering Pipelines for Optimized Production of Renewable Chemicals. Frontiers in Bioengineering and Biotechnology, 2021, 9, 673005.	4.1	14
72	Local Mutations Can Serve as a Game Changer for Global Protein Solvent Interaction. Jacs Au, 2021, 1, 1076-1085.	7.9	14

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73	Assigning transmembrane segments to helices in intermediate-resolution structures. Bioinformatics, 2004, 20, i122-i129.	4.1	13
74	Incorporating an allosteric regulatory site in an antibody through backbone design. Protein Science, 2017, 26, 807-813.	7.6	13
75	Overcoming a species-specificity barrier in development of an inhibitory antibody targeting a modulator of tumor stroma. Protein Engineering, Design and Selection, 2016, 29, 135-147.	2.1	12
76	One-step sequence and structure-guided optimization of HIV-1 envelope gp140. Current Research in Structural Biology, 2020, 2, 45-55.	2.2	12
77	The neutralization potency of anti-SARS-CoV-2 therapeutic human monoclonal antibodies is retained against viral variants. Cell Reports, 2021, 36, 109679.	6.4	12
78	Combined Crystal Structure of a Type I Cohesin. Journal of Biological Chemistry, 2015, 290, 16215-16225.	3.4	10
79	Inspired by nature. Science, 2016, 352, 657-658.	12.6	10
80	pANT: A Method for the Pairwise Assessment of Nonfunctionalization Times of Processed Pseudogenes. Molecular Biology and Evolution, 2003, 20, 1876-1880.	8.9	9
81	Computational protein design suggests that human PCNAâ€partner interactions are not optimized for affinity. Proteins: Structure, Function and Bioinformatics, 2013, 81, 341-348.	2.6	9
82	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.	2.1	8
83	Directâ€MS analysis of antibodyâ€antigen complexes. Proteomics, 2021, 21, e2000300.	2.2	8
84	A Rationally and Computationally Designed Fluorescent Biosensor for <scp>d</scp>-Serine. ACS Sensors, 2021, 6, 4193-4205.	7.8	8
85	Stabilization of the SARS-CoV-2 receptor binding domain by protein core redesign and deep mutational scanning. Protein Engineering, Design and Selection, 2022, 35, .	2.1	8
86	Computationally designed hyperactive Cas9 enzymes. Nature Communications, 2022, 13, .	12.8	8
87	Design of a basiginâ€mimicking inhibitor targeting the malaria invasion protein RH5. Proteins: Structure, Function and Bioinformatics, 2020, 88, 187-195.	2.6	6
88	What Have We Learned from Design of Function in Large Proteins?. Biodesign Research, 2022, 2022, .	1.9	6
89	Biomolecular Recognition of the Glycan Neoantigen CA19-9 by Distinct Antibodies. Journal of Molecular Biology, 2021, 433, 167099.	4.2	5
90	Computer-aided engineering of staphylokinase toward enhanced affinity and selectivity for plasmin. Computational and Structural Biotechnology Journal, 2022, 20, 1366-1377.	4.1	4

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91	Highly Specific Monoclonal Antibody Targeting the Botulinum Neurotoxin Type E Exposed SNAP-25 Neoepitope. Antibodies, 2022, 11, 21.	2.5	4
92	Editorial overview: Protein design and evolutionâ€"new protein architectures, evolutionary fine-tuning and analysis. Current Opinion in Structural Biology, 2015, 33, v-vi.	5.7	0