Julia M Shifman

List of Publications by Year
in descending order

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40 papers	1,426 citations	430874 18 h-index	345221 36 g-index
43 all docs	43 docs citations	43 times ranked	1692 citing authors

#	Article	IF	Citations
1	Transfer-PCR (TPCR): A highway for DNA cloning and protein engineering. Journal of Structural Biology, 2011, 175, 171-177.	2.8	124
2	Computational design of an integrin I domain stabilized in the open high affinity conformation. Nature Structural Biology, 2000, 7, 674-678.	9.7	123
3	Ca2+/calmodulin-dependent protein kinase II (CaMKII) is activated by calmodulin with two bound calciums. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13968-13973.	7.1	122
4	Exploring the origins of binding specificity through the computational redesign of calmodulin. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13274-13279.	7.1	107
5	Modulating Calmodulin Binding Specificity through Computational Protein Design. Journal of Molecular Biology, 2002, 323, 417-423.	4.2	105
6	How Structure Defines Affinity in Protein-Protein Interactions. PLoS ONE, 2014, 9, e110085.	2.5	77
7	Development of High Affinity and High Specificity Inhibitors of Matrix Metalloproteinase 14 through Computational Design and Directed Evolution. Journal of Biological Chemistry, 2017, 292, 3481-3495.	3.4	64
8	What Makes Ras an Efficient Molecular Switch: A Computational, Biophysical, and Structural Study of Ras-GDP Interactions with Mutants of Raf. Journal of Molecular Biology, 2010, 399, 422-435.	4.2	58
9	Tradeoff Between Stability and Multispecificity in the Design of Promiscuous Proteins. PLoS Computational Biology, 2009, 5, e1000627.	3.2	54
10	Computational Design of Calmodulin Mutants with up to 900-Fold Increase in Binding Specificity. Journal of Molecular Biology, 2009, 385, 1470-1480.	4.2	51
11	Multispecific Recognition: Mechanism, Evolution, and Design. Biochemistry, 2011, 50, 602-611.	2.5	47
12	Affinity- and Specificity-Enhancing Mutations Are Frequent in Multispecific Interactions between TIMP2 and MMPs. PLoS ONE, 2014, 9, e93712.	2.5	43
13	Dead-end elimination for multistate protein design. Journal of Computational Chemistry, 2007, 28, 2122-2129.	3.3	41
14	Protein Engineering by Combined Computational and In Vitro Evolution Approaches. Trends in Biochemical Sciences, 2016, 41, 421-433.	7.5	38
15	Saturation scanning of ubiquitin variants reveals a common hot spot for binding to USP2 and USP21. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8705-8710.	7.1	36
16	Converting a broad matrix metalloproteinase family inhibitor into a specific inhibitor of <scp>MMP</scp>â€9 and <scp>MMP</scp>â€14. FEBS Letters, 2018, 592, 1122-1134.	2.8	31
17	Cold Spots in Protein Binding. Trends in Biochemical Sciences, 2016, 41, 739-745.	7.5	24
18	Triathlon for energy functions: Who is the winner for design of proteinâ€“protein interactions?. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1487-1498.	2.6	22

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19	RAS/Effector Interactions from Structural and Biophysical Perspective. Mini-Reviews in Medicinal Chemistry, 2016, 16, 370-375.	2.4	21
20	Computational Methods for Controlling Binding Specificity. Methods in Enzymology, 2013, 523, 41-59.	1.0	20
21	Predicting affinity- and specificity-enhancing mutations at proteinâ€“protein interfaces. Biochemical Society Transactions, 2013, 41, 1166-1169.	3.4	20
22	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. Journal of Molecular Biology, 2019, 431, 336-350.	4.2	20
23	A Single-Tube Assembly of DNA Using the Transfer-PCR (TPCR) Platform. Methods in Molecular Biology, 2014, 1116, 89-101.	0.9	20
24	Optimizing energy functions for proteinâ€“protein interface design. Journal of Computational Chemistry, 2011, 32, 23-32.	3.3	19
25	RASSF effectors couple diverse RAS subfamily GTPases to the Hippo pathway. Science Signaling, 2020, 13, .	3.6	19
26	Mapping of the Binding Landscape for a Picomolar Protein-Protein Complex through Computation and Experiment. Structure, 2014, 22, 636-645.	3.3	18
27	Combinatorial and Computational Approaches to Identify Interactions of Macrophage Colony-stimulating Factor (M-CSF) and Its Receptor c-FMS. Journal of Biological Chemistry, 2015, 290, 26180-26193.	3.4	18
28	Alteration of the C-Terminal Ligand Specificity of the Erbin PDZ Domain by Allosteric Mutational Effects. Journal of Molecular Biology, 2014, 426, 3500-3508.	4.2	17
29	Design, expression and characterization of mutants of fasciculin optimized for interaction with its target, acetylcholinesterase. Protein Engineering, Design and Selection, 2009, 22, 641-648.	2.1	13
30	Climbing Up and Down Binding Landscapes through Deep Mutational Scanning of Three Homologous Proteinâ€“Protein Complexes. Journal of the American Chemical Society, 2021, 143, 17261-17275.	13.7	11
31	Generating quantitative binding landscapes through fractional binding selections combined with deep sequencing and data normalization. Nature Communications, 2020, 11, 297.	12.8	10
32	Analysis of Structural Features Contributing to Weak Affinities of Ubiquitin/Protein Interactions. Journal of Molecular Biology, 2017, 429, 3353-3362.	4.2	8
33	Identifying Residues that Determine SCF Molecular-Level Interactions through a Combination of Experimental and In silico Analyses. Journal of Molecular Biology, 2017, 429, 97-114.	4.2	8
34	Computational design and experimental optimization of protein binders with prospects for biomedical applications. Protein Engineering, Design and Selection, 2021, 34, .	2.1	7
35	Synthetic peptides mimicking the binding site of human acetylcholinesterase for its inhibitor fasciculin 2. Journal of Peptide Science, 2015, 21, 723-730.	1.4	6
36	Engineered variants of the Ras effector protein RASSF5 (NORE1A) promote anticancer activities in lung adenocarcinoma. Journal of Biological Chemistry, 2021, 297, 101353.	3.4	2

#	Article	IF	Citations
37	Intricacies of Î² Sheet Protein Design. Structure, 2008, 16, 1751-1752.	3.3	1
38	Predicting the consequences of mutations. , 2020, , 145-165.		1
39	Editorial overview: Engineering and design: New trends in designer proteins. Current Opinion in Structural Biology, 2017, 45, iv-vi.	5.7	0
40	A KLK4 proteinase substrate capture approach to antagonize PAR1. Scientific Reports, 2021, 11, 16170.	3.3	0