Julia M Shifman

List of Publications by Year
in descending order

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	A KLK4 proteinase substrate capture approach to antagonize PAR1. Scientific Reports, 2021, 11, 16170.	3.3	0
2	Computational design and experimental optimization of protein binders with prospects for biomedical applications. Protein Engineering, Design and Selection, 2021, 34, .	2.1	7
3	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
4	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
5	RASSF effectors couple diverse RAS subfamily GTPases to the Hippo pathway. Science Signaling, 2020, 13, .	3.6	19
6	Generating quantitative binding landscapes through fractional binding selections combined with deep sequencing and data normalization. Nature Communications, 2020, 11, 297.	12.8	10
7	Predicting the consequences of mutations. , 2020, , 145-165.		1
8	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. Journal of Molecular Biology, 2019, 431, 336-350.	4.2	20
9	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
10	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
11	Editorial overview: Engineering and design: New trends in designer proteins. Current Opinion in Structural Biology, 2017, 45, iv-vi.	5.7	0
12	Analysis of Structural Features Contributing to Weak Affinities of Ubiquitin/Protein Interactions. Journal of Molecular Biology, 2017, 429, 3353-3362.	4.2	8
13	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
14	RAS/Effector Interactions from Structural and Biophysical Perspective. Mini-Reviews in Medicinal Chemistry, 2016, 16, 370-375.	2.4	21
15	Protein Engineering by Combined Computational and In Vitro Evolution Approaches. Trends in Biochemical Sciences, 2016, 41, 421-433.	7.5	38
16	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
17	Cold Spots in Protein Binding. Trends in Biochemical Sciences, 2016, 41, 739-745.	7.5	24
18	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

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19	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
20	Affinity- and Specificity-Enhancing Mutations Are Frequent in Multispecific Interactions between TIMP2 and MMPs. PLoS ONE, 2014, 9, e93712.	2.5	43
21	Mapping of the Binding Landscape for a Picomolar Protein-Protein Complex through Computation and Experiment. Structure, 2014, 22, 636-645.	3.3	18
22	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
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	How Structure Defines Affinity in Protein-Protein Interactions. PLoS ONE, 2014, 9, e110085.	2.5	77
25	Computational Methods for Controlling Binding Specificity. Methods in Enzymology, 2013, 523, 41-59.	1.0	20
26	Predicting affinity- and specificity-enhancing mutations at proteinâ€“protein interfaces. Biochemical Society Transactions, 2013, 41, 1166-1169.	3.4	20
27	Multispecific Recognition: Mechanism, Evolution, and Design. Biochemistry, 2011, 50, 602-611.	2.5	47
28	Transfer-PCR (TPCR): A highway for DNA cloning and protein engineering. Journal of Structural Biology, 2011, 175, 171-177.	2.8	124
29	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
30	Optimizing energy functions for proteinâ€“protein interface design. Journal of Computational Chemistry, 2011, 32, 23-32.	3.3	19
31	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
32	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
33	Tradeoff Between Stability and Multispecificity in the Design of Promiscuous Proteins. PLoS Computational Biology, 2009, 5, e1000627.	3.2	54
34	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
35	Intricacies of Î² Sheet Protein Design. Structure, 2008, 16, 1751-1752.	3.3	1
36	Dead-end elimination for multistate protein design. Journal of Computational Chemistry, 2007, 28, 2122-2129.	3.3	41

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37	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
38	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
39	Modulating Calmodulin Binding Specificity through Computational Protein Design. Journal of Molecular Biology, 2002, 323, 417-423.	4.2	105
40	Computational design of an integrin I domain stabilized in the open high affinity conformation. Nature Structural Biology, 2000, 7, 674-678.	9.7	123