

Kimberly A Reynolds

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,112
citations

643344

15
h-index

799663

21
g-index

32
all docs

32
docs citations

32
times ranked

1815
citing authors

#	ARTICLE	IF	CITATIONS
1	Accelerating Biological Insight for Understudied Genes. Integrative and Comparative Biology, 2021, , .	0.9	2
2	Structurally distributed surface sites tune allosteric regulation. ELife, 2021, 10, .	2.8	23
3	A simplified strategy for titrating gene expression reveals new relationships between genotype, environment, and bacterial growth. Nucleic Acids Research, 2021, 49, e6-e6.	6.5	14
4	Strategies for Engineering and Rewiring Kinase Regulation. Trends in Biochemical Sciences, 2020, 45, 259-271.	3.7	16
5	Altered expression of a quality control protease in E. coli reshapes the in vivo mutational landscape of a model enzyme. ELife, 2020, 9, .	2.8	37
6	A Two-Enzyme Adaptive Unit within Bacterial Folate Metabolism. Cell Reports, 2019, 27, 3359-3370.e7.	2.9	27
7	High-Order Epistasis in Catalytic Power of Dihydrofolate Reductase Gives Rise to a Rugged Fitness Landscape in the Presence of Trimethoprim Selection. Molecular Biology and Evolution, 2019, 36, 1533-1550.	3.5	52
8	An evolutionary hotspot defines functional differences between CRYPTOCHROMES. Nature Communications, 2018, 9, 1138.	5.8	72
9	Engineering allosteric regulation in protein kinases. Science Signaling, 2018, 11, .	1.6	18
10	An evolution-based strategy for engineering allosteric regulation. Physical Biology, 2017, 14, 025002.	0.8	13
11	Conserved amino acid networks modulate discrete functional properties in an enzyme superfamily. Scientific Reports, 2017, 7, 3207.	1.6	35
12	Evolution-Based Functional Decomposition of Proteins. PLoS Computational Biology, 2016, 12, e1004817.	1.5	119
13	A New Test of Computational Protein Design: Predicting Posttranslational Modification Specificity for the Enzyme SMYD2. Structure, 2015, 23, 11-12.	1.6	1
14	Finding a Common Path: Predicting Gene Function using Inferred Evolutionary Trees. Developmental Cell, 2014, 30, 4-5.	3.1	0
15	Evolution-Based Design of Proteins. Methods in Enzymology, 2013, 523, 213-235.	0.4	37
16	Hot Spots for Allosteric Regulation on Protein Surfaces. Cell, 2011, 147, 1564-1575.	13.5	311
17	Specificity and cooperativity at Î²â€lactamase position 104 in TEMâ€1/BLIP and SHVâ€1/BLIP interactions. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1267-1276.	1.5	15
18	Analysis of full and partial agonists binding to <i>Î²</i>₂-adrenergic receptor suggests a role of transmembrane helix V in agonistâ€specific conformational changes. Journal of Molecular Recognition, 2009, 22, 307-318.	1.1	113

#	ARTICLE	IF	CITATIONS
19	Identifying conformational changes of the β_2 adrenoceptor that enable accurate prediction of ligand/receptor interactions and screening for GPCR modulators. <i>Journal of Computer-Aided Molecular Design</i> , 2009, 23, 273-288.	1.3	60
20	Computational Redesign of the SHV-1 β -Lactamase/ β -Lactamase Inhibitor Protein Interface. <i>Journal of Molecular Biology</i> , 2008, 382, 1265-1275.	2.0	40
21	An object-oriented library for computational protein design. <i>Journal of Computational Chemistry</i> , 2007, 28, 2378-2388.	1.5	34
22	Structural and Computational Characterization of the SHV-1 β -Lactamase- β -Lactamase Inhibitor Protein Interface. <i>Journal of Biological Chemistry</i> , 2006, 281, 26745-26753.	1.6	46