

Eyal Akiva

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,685
citations

687363

13
h-index

713466

21
g-index

23
all docs

23
docs citations

23
times ranked

3247
citing authors

#	ARTICLE	IF	CITATIONS
1	Human SIRT1 Multispecificity Is Modulated by Active-Site Vicinity Substitutions during Natural Evolution. <i>Molecular Biology and Evolution</i> , 2021, 38, 545-556.	8.9	5
2	Parallel molecular mechanisms for enzyme temperature adaptation. <i>Science</i> , 2021, 371, .	12.6	48
3	Structural, Kinetic, and Mechanistic Analysis of an Asymmetric 4-Oxalocrotonate Tautomerase Trimer. <i>Biochemistry</i> , 2019, 58, 2617-2627.	2.5	6
4	Exploring the sequence, function, and evolutionary space of protein superfamilies using sequence similarity networks and phylogenetic reconstructions. <i>Methods in Enzymology</i> , 2019, 620, 315-347.	1.0	13
5	A global view of structure–function relationships in the tautomerase superfamily. <i>Journal of Biological Chemistry</i> , 2018, 293, 2342-2357.	3.4	39
6	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a “Plug and Play” Domain. <i>Methods in Enzymology</i> , 2018, 606, 1-71.	1.0	99
7	Revealing Unexplored Sequence-Function Space Using Sequence Similarity Networks. <i>Biochemistry</i> , 2018, 57, 4651-4662.	2.5	58
8	Biocuration in the structure–function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	6
9	Evaluating Functional Annotations of Enzymes Using the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 111-132.	0.9	14
10	Evolutionary and molecular foundations of multiple contemporary functions of the nitroreductase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9549-E9558.	7.1	111
11	Biocuration in the structure–function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	2
12	Evolutionary Reprogramming of Protein-Protein Interaction Specificity. <i>Cell</i> , 2015, 163, 535-537.	28.9	1
13	Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere. <i>PLoS Biology</i> , 2014, 12, e1001843.	5.6	79
14	The Structure–Function Linkage Database. <i>Nucleic Acids Research</i> , 2014, 42, D521-D530.	14.5	210
15	Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks. <i>ELife</i> , 2014, 3, .	6.0	81
16	Prediction of Mutational Tolerance in HIV-1 Protease and Reverse Transcriptase Using Flexible Backbone Protein Design. <i>PLoS Computational Biology</i> , 2012, 8, e1002639.	3.2	21
17	Global landscape of HIV–human protein complexes. <i>Nature</i> , 2012, 481, 365-370.	27.8	651
18	A Dynamic View of Domain-Motif Interactions. <i>PLoS Computational Biology</i> , 2012, 8, e1002341.	3.2	48

#	ARTICLE	IF	CITATIONS
19	Preferential use of protein domain pairs as interaction mediators: order and transitivity. <i>Bioinformatics</i> , 2010, 26, 2564-2570.	4.1	11
20	Built-in loops allow versatility in domain-domain interactions: Lessons from self-interacting domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13292-13297.	7.1	86
21	Evolutionary conservation of domain-domain interactions. <i>Genome Biology</i> , 2006, 7, R125.	9.6	96